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From:

Marvich, Maria

Sent:

Thursday, January 12, 2006 2:01 PM

To:

STIC-Biotech/ChemLib

Subject:

09/729658

Please search SEQ ID NO:2 including interference. (391 amino acids)

Maria Bonovich Marvich, PhD

United States Patent and Trademark Office

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Online Time:

Type of Search

NA#______ AA#:____

S/L:____ Oligomer:____

Encode/Transl:_____

Structure #:_____Text:___

Inventor:_____ Litigation:____

Vendors and cost where applicable STN:

DIALOG:
QUESTEL/ORBIT:
LEXIS/NEXIS:
SEQUENCE SYSTEM:
WWW/Internet:
Other (Specify):

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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases: older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions .rnpbm (Published_Applications_NA_New).

Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions .rapbm (Published_Applications_AA_New).

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GenCore version 5.1.6 (c) 1993 - 2006 Compugen Ltd. Copyright

- protein search, using sw model OM protein January 13, 2006, 16:06:11 Run on:

; Search time 79 Seconds (without alignments) 2174.647 Million cell updates/sec

Title: Perfect score:

US-09-729-658C-2 2098 1 MGYPEVERRELLPAAAPRER......NMSKHTTFFGAIRLGEAPAS 391 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

residues 2443163 seqs, 439378781 Searched:

2443163 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Minimum Match 0% Maximum Match 100% Listing first 45 summaries Post-processing:

geneseqp2003as:*geneseqp2003bs:*geneseqp2004s:*geneseqp2005s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp1980s:* geneseqp1990s:* A_Geneseq Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Abp53104 Human ect	Abb09082 Human EDA	Abr42324 Human EDA	Abo01928 Human EDA	Adc35224 Human TNF	_	Adx06863 Cyclin-de	Abb09083 Mouse Tab	_	Adp75164 Fusion co	Adp75166 Fusion co	Aaw44764 Human anh		_	_	Aab72738 Repetitiv	_	Aag63347 Amino aci	Mouse	Ad191062 Mouse col	Aar53257 Human col	Ade55566 Human Pro	Ade55570 Human Pro	Adp65220 Human alp
QI	ABP53104	ABB09082	ABR42324	ABO01928	ADC35224	ABW02286	ADX06863	ABB09083	AB001929	ADP75164	ADP75166	AAW44764	AAR95115	AAW57646	AAB64008	AAB72738	ADL91066	AAG63347	ADL91057	ADL91062	AAR53257	ADE55566	ADE55570	ADP65220
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280.5	280.5	280.5	277	277	277	277	276	276	275	275	273.5	273	273	273	273	273	273	273	272	268.5
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ALIGNMENTS

ABP53104 standard; protein; 391 AA RESULT 1 ABP53104

ABP53104;

(first entry) 11-NOV-2002 Human ectodermal dysplasia protein (EDA) SEQ ID NO:6.

Human; adipocyte complement related protein; zacrp3x2; antiinflammatory; vasotropic; antimicrobial; vulnerary; antiarteriosclerotic; gene thorapy; adipogenesis; glucosequesis; glucosequesis; glucose uptake; protein synthesis; thermogenesis; oxygen utiliaation; inflammation; neurotransmitter; antimicrobial; infection.

Homo sapiens.

WO200246417-A2.

13-JUN-2002.

07-DEC-2001; 2001WO-US047348.

07-DEC-2000; 2000US-0254019P.

(ZYMO) ZYMOGENETICS INC.

Sheppard PO; Thayer BC, Haldeman BA,

WPI; 2002-657398/70.

for useful due to Novel human adipocyte complement related protein, zacrp3x2, modulating energy balance in mammals, and preventing injury ischemia/inflammation.

Disclosure, Page 111-112; 118pp, English.

The present invention describes a human adipocyte complement related protein (I) designated zacrp3x2. (I) has antinflammatory, vasotropic, antimicrobial, vulnerary and antiarteriosclerotic activities, and can be used in somatic cell gene therapy, and as a modulator of neurotransmission. (I) is useful for modulating energy balance in mammals or for protecting endothelial cells from injury, for modulating cellular metabolic reactions e.g. adipogenesis, gluconeogenesis, glycogenolygis, lipogenesis, glucose uptake, protein synthesis, thermogenesis and oxygen utilisation, for surgical pretreatment to prevent injury due to ischaemia

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WPI; 2002-360478/39. N-PSDB; ABL51009. Zonana J, Ferguson

(BAYU) BAYLOR COLLEGE MEDICINE. (UYOR-) UNIV OREGON HEALTH SCI.

98US-0092279P. 98US-0112366P.

09-JUL-1998; 15-DEC-1998;

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contransmission e.g., modulates calcium ion concentration, muscle neurotransmission e.g., modulates calcium ion concentration, muscle contraction, hormone separation, DNA synthesias or cell growth, inositol phosphate turnover, arachidonate release, phospholipase-C activation, gastric emptying, human neutrophil activation or superoxide anion production, for modulating nutrient uptake e.g. 2-deoxy-glucose uptake in the brain, sa anti-microbial agent, as cell culture reagents in vitro studies of exogenous microorganism infection such as bacterial, viral or fungal infection, as in vivo animal models of infection, for promoting platelets that adhere and are activated and the size of platelet capters. Human zacrp3x2 is located on chromosome 5, more appecifically to chromosome 5pl2-pl3.3. The present sequence represents human cacrp3x2 is cateded and chromosome 5, more appecifically contomer inventor.
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Best Local Similarity 100.
Matches 391, Conservative
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The present invention describes a purified hypohidrotic ectodermal dysplasias protein (I) that promotes the development of hair follicles.

(I) is a promoter of hair follicle growth and tooch growth. (I) is useful for the development of hair follicles. (I) is also useful for commercial and clinical diagnostic testing for ectodermal dysplasia (ED). (I) is also useful as a stimulant for hair and tooth growth, for stimulating endocrine sweat gland development in individuals from whom the normal sweating mechanism is compromised by disease or surgery, for stimulating the growth of mammary epithelial tissue, either for reconstructing or cosmetic purposes, and for promoting or maintaining differentiation of breast epithelium. (I) is also useful for functional analysis, antibody production and patient therapy. ABLS1009 to ABLS1122 and ABB09082 to
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11-AUG-2003

Homo sapiens

15-MAY-2003

Hilbert DH,

osteopathic.

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The invention relates to a method of increasing or decreasing one or more of hair follicle development, tooth development, or sweat gland development, in a tissue, involves altering ectodermal dysplasia (BDA1) isoform II (EDA1-II) activity in the tissue. The method is useful for increasing or decreasing hair follicle development, tooth development or sweat gland development, in a tissue of a patient usifering from an ectodermal disease such as X-linked hypohidrotic ectodermal dysplasia (XLHED), autosommal recessive hypohidrotic ectodermal dysplasia alopecia. The method is useful for decreasing hair follicle development in a subject suffering from hirsutism. The method is also useful for the setting breast cancer and ectogic teeth, burns and trauma of skin due to surgery. The present sequence represents the amino acid sequence of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 YLELRSELRRERGAESRLGGSGTPGTSGTLSSLGGLDPDSPITSHLGQPSPKQQPLEPGE 120
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                                                                                                                                                                                                                                                                                                     Human; BDA1-II; hair follicle development; tooth development; rauma; bus sweat gland development; ectodermal disease; alopecia; skin trauma; bus X-linked hypohidrotic ectodermal dysplasia; XLHED; breast cancer; HBD; autosomal recessive hypohidrotic ectodermal dysplasia; hirsutism;
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100.0%; Pred. No. 5.9e-155;
ive 0; Mismatches 0;
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AVKAVHADISINMSKHTTFFGAIRLGEAPAS 391
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98US-0112366P.
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29-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is the protein sequence of human EDA polypeptide. The invention relates to compositions comprising hererotrimeric complexes of tumour necrosis factor (TNF) ligand family members, and their use in the detection, prevention and treatment of disease. In preferred embodiments, the heterotrimeric complex comprises full-length or extracellular portions of EDA together with full-length or extracellular portions of other TNF ligand family members. The heterotrimeric complexes of the invention are useful for treating an autoimmune disease, cancer osteoporosis, and particularly for inhibiting cancer cell proliferation, increasing B cell proliferation, or inducing apoptosis of T cells
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                                                                                            necrosis factor; ligand; cytostatic; immunomodulator;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 387-388; 388pp; English
                                                                                                                                                                                                                                                                                         25-JUL-2002; 2002WO-US023782
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         (first entry)
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N-PSDB; ACC57910.
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                                                                                                   tumour
                                                   Human EDA protein
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comprises administering an endokine alpha antagonist, which is the antibody that binds specifically to endokine alpha polypeptide. The present sequence represents the amino acid sequence of a tumour necrosis factor family ligand.
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                                                                                                                                                                                                    121 AALHSDSQDGHQMALLINFFFPDEKPYSEEESRRVRRNKRSKSNEGADGPVKNKKKKKAG
                                                                                                                                                                                                                                                      PPGPNGPPGPPGPPGTPGTPGTPGTTVMGPPGPPGPPGPPGPPGLQGPSGAADK
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                                                                                                                                                                                                                                                                                                                                                                                                     61 YLELRSELRRERGAESRLGGSGTPGTSGTLSSLGGLDPDSPITSHLGQPSPKQQPLEPGE
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                                                                                                                                       1 MGYPEVERRELLPAAAPRERGSQGCGCGGAPARAGEGNSCLLFLGFFGLSLALHLLTLCC
                                                                                         Length 391;
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100.0%; Pred. No. 5.9e-155;
ive 0; Mismatches 0;
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95US-00461246.
98US-00006220.
98US-00131237.
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                                                                                                                    Matches 391; Conservative
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                                                                    Sequence 391 AA
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05-JUN-1995;
09-JAN-1998;
07-REB-1998;
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13-MAY-1999;
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         New Endokine alpha gene useful for preparing a composition for treating disease associated with excessive or insufficient bone resorption e.g., osteoporosis, Paget's disease or arterial calcification.
                                                            PPGPNGPPGPPGPPGPPGIPGIPGIPGIPGTTVMGPPGPPGPPGPPGPPGLPGPSAADK
                                                                                                                                                                YPIYSQVEVYYINFTDFASYEVVVDEKPFLQCTRSIETGKTNYNTCYTAGVCLLKARQKI
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                                                                                                                                              AGTRENQPAVVHLQGQGSAIQVKNDLSGGVLNDWSRITMNPKVFKLHPRSGELEVLVDGT
                                                                                                                                                                                                                                                                                                                                                                                                                               human; tumour necrosis factor; TNF ligand; endokine alpha; excessive bone resorption disorder; osteoporosis; Paget's disease; arterial calcification.
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(NIJJ/) NI J.
(ROSE/) ROSEN C A.
(NARD/) NARDELLI B.
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                                                                                                                                                                                                                                                                                                                                                                                                     sequence is human
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                                                                                                                                                                                                                                                                                          The invention relates to methods and compositions for treating or ameliorating a disease or disorder of the gastrointestinal tract. The method involves administering a composition comprising tumour necrosis factor (TNF)-gamma-beta and its receptors DR3 and TR6 to a person with or suspected of having the disease or disorder. The antagonist of TNF-gamma-beta is useful for treating or ameliorating a gastrointestinal tract disease or disorder, specifically an inflammatory bowel disease, e.g. Crohn's disease or ulcarative colitis. The present sequence is hum a protein. This sequence is used to illustrate the method of the
                                                                                                                                                                                                     Use of tumor necrosis factor gamma-beta antagonists for treating or ameliorating a disease or disorders of the gastrointestinal tract, e.g. inflammatory bowel disease, Crohn's disease or ulcerative colitis.
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                                                                                                                                Zhang J,
            26-MAR-2001; 2001US-0278449F.
06-UUL-2001; 2001US-00899059.
24-AUG-2001; 2001US-031438IP.
07-DEC-2001; 2001US-035695F.
23-AUG-2002; 2002US-00226294.
                                                                                                     (HUMA-) HUMAN GENOME SCI
                                                                                                                                  Rosen CA,
                                                                                                                                                            WPI; 2003-852773/79.
N-PSDB; AAD63922.
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whether a mammal will respond or is responding to an anti-cancer agent that modulates cyclin-dependent kinase (cdk) activity. The method comparises measuring the level of one or more blomarkers selected from 2774 biomarkers given in the specification (nucleotide sequence SEQ ID No.1246 (Genbank EST W28729) is especially preferred). The method of the invention is utilized in a kit for determining or predicting whether patient would be susceptible or resistant to treatment by an agent modulating cdk activity. The invention also describes a method for utilizing individualized genetic profiles for treating diseases and disorders based on patient's response and molecular level, specialized microarrays comprising the biomarkers described, antibodies directed against the biomarkers and a cell culture model to identify blomarkers. The cdk modulator is preferably N-5-[[5-(1,1-1-Dimethylethyl)-2-oxazolyl] methyllthiol-2-thiazolyl-4-piperidine carboxamide, 0.5-Loxazolyl] methyllthiol-2-thiazolyl-4-piperidine carboxamide, 0.5-Loxazolyl methyllthiol-2-thiazolyl-4-piperidine carboxamide in electronic format directly from WIPO at ftp.wipo.inft/pub/published_pct_sequences. This sequence represents a biomarker used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mammal
cyclin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 YLELRSELRRERGAESRLGGSGTPGTSGTLSSLGGLDPDSPITSHLGQPSPRQQPLRPGB 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention describes a novel method of predicting or determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biomarkers useful for predicting or determining the response of a to a cancer treatment comprising administration of a modulator of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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1428
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2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wong TW;
                                                               cytostatic; cyclin-dependent kinase; cdk; biomarker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 2098; DB 9;
100.0%; Pred. No. 5.9e-155;
iive 0; Mismatches 0;
Cyclin-dependent kinase modulation biomarker SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Webster KR, Jackson DG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5; SEQ ID NO 1428; 141pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BRIM ) BRISTOL-MYERS SQUIBB
                                                                                                                                                                                                                                                                                                                                                               29-JUL-2004; 2004WO-US024424
                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JUL-2003; 2003US-0490890P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to a cancer treatment comp
dependent kinase activity.
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Matches 391; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2005-163068/17.
N-PSDB; ADX06862.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rupnow BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 391 AA;
                                                                                                                                                                                                                     WO2005012875-A2
                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
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180 180

181 PPGPNGPPGPPGPPGPPGIPGIPGIPGIPGTTVMGPPGPPGPPGPGGPPGLQGPSGAADK

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standard; protein; 391

ADX06863

ADX06863

21-APR-2005 (first entry)

ADX06863;

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AGTRENOPAVVHLOGOGSAI OVKNDLSGGVLNDWSRITMNPKVFKLHPRSGBLEVLVDGT

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1 VIELRSELRRERGTESRLGGPGAPGTSGTLSSPGSLDPVGPITRHLGQPSPQQQPLEPGE
                                                                              YLELRSELRRERGAESRLGGSGTPGTSGTLSSLGGLDPDSPITSHLGQPSPKQQPLEPGE
                                                                                                                           PPGPNGPPGPPGPPGPPGIPGIPGIPGTTVMGPPGPPGPPGPPGPPGLQGPSGAADK
                                                                                                                                             121 AALHSDSQDGHQMALLNFFFPDEKPYSEESRRVRRNKRSKSNEGADGPVKNKKKGKKAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-AUG-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zonana J, Ferguson BM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ZONA/) ZONANA J.
(FERG/) FERGUSON B M.
(HEAD/) HEADON D.
(OVER/) OVERBEEK P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-456312/43.
N-PSDB; ACD07896.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse Ta protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ectopic teeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-JUL-1998;
15-DEC-1998;
29-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2003
                                                                                                                                                                                                                                                                                         294
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ABO01929
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a purified hypohidrotic ectodermal dysplasias protein (1) that promotes the development of hair follicles. (1) is a promoter of hair follicle growth and cooth growth. (1) is useful for the development of hair follicles (1) is also useful for commercial and clinical diagnostic testing for ectodermal dysplasia (ED). (1) is also useful as a stimulant for hair and tooth growth, for stimulating endocrine sweat gland development in individuals from whom the normal sweating mechanism is compromised by disease or surgery, for stimulating the growth of mammary epithelial tissue, either for reconstructing or cosmetic purposes, and for promoting or maintaining differentiation of breast epithelium. (1) is also useful for functional analysis, antibody production and patient therapy. ABL51009 to ABL51122 and ABB09082 to
                                                                                                                                                                                                                                                                                                        Human; mouse; EDA1-II; X-linked hypohidrotic ectodermal dysplasia; XLHED; DL receptor; DL gene; downless gene; ectodermal dysplasia; hair follicle growth; tooth growth; endocrine sweat gland development; mammary epithelial tissue growth; breast epithelium.
                       301 YFIYSQVEVYYINFIDFASYEVVVDEKPFLQCTRSIETGKTNYNTCYTAGVCLLKARQKI 360
    YFIYSQVEVYXINFTDFASYEVVVDEKPFLQCTRSIETGKTNYNTCYTAGVCLLKARQKI 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MGYPEVERRELLPAAAPRERGSQGCGCGGAPARAGEGNSCLLFLGFFGLSLALHLLTLCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel purified hypohidrotic ectodermal dysplasias protein, useful for promoting the development of hair follicles and tooth growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1873; DB 5;
Pred. No. 1.9e-137;
2; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Headon D, Overbeek
                                                                                      361 AVKAVHADISINMSKHTTFFGAIRLGEAPAS 391
                                                                    AVKMVHADISINMSKHTTFFGAIRLGEAPAS 391
                                                                                                                                                                                                                                                                             Mouse Tabby (Ta) protein SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Col 71-74; 86pp; English.
                                                                                                                                                                                ABB09083 standard; protein; 377 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BAYU ) BAYLOR COLLEGE MEDICINE. (UYOR-) UNIV OREGON HEALTH SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0092279P.
98US-0112366P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 90.8%;
Matches 355; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-00342681.
                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zonana J, Ferguson BM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002-360478/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABL51010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 377 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-MAR-2002.
                                                                                                                                                                                                                                               26-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nvention
                                                                                                                                                                                                                ABB09083;
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                                                                                                                                                  RESULT 8
ABB09083
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241 AGTRENOPAVVHLOGGGSALQVKNDLSGGVLNDWSRITMNPKVFKLHPRSGELEVLVDGT 300
                               293
                                                                                                                                                                                                                                                                                                                                                   Mouse, Tabby, hair follicle development; tooth development; Ta; sweat gland development; ectodermal disease; alopecia; skin trauma; burn; X-linked hypohidrotic ectodermal dysplasia; XLHED; breast cancer; HED; autosomal recessive hypohidrotic ectodermal dysplasia; hirsutism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method of increasing or decreasing one or mo. of hair follicle development, tooth development, or sweat gland development, in a tissue, involves altering ectodermal dysplasia (EDA1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Increasing or decreasing hair follicle development, tooth development, sweat gland development, in a tissue, involves modulating ectodermal dysplasia protein isoform II activity in the tissue.
                  241 TGTRENQPAVVHLQGQGSAIQVKNDLSGGVLNDWSRITWNPKVFKLHPRSGEL-----
                                                                                -----EVYYINFTDFASYEVVVDEKPFLQCTRSIETGKTNYNTCYTAGVCLLKARQKI
                                                               301 YPIYSQVEVYYINFIDFASYEVVVDEKPFLQCTRSIETGKTNYNTCYTAGVCLLKARQKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Overbeek P;
                                                                                                                         361 AVKMVHADISINMSKHTTFFGAIRLGEAPAS 391
                                                                                                                                            347 AVKWVHADISINMSKHTTFFGAIRLGBAPAS 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Headon D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Fig 1; 102pp; English.
                                                                                                                                                                                                                                    ABO01929 standard; protein; 377
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98US-0112366P.
99US-00342681.
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/note= "hED1 aa245-391"

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isoform II (EDA1-II) activity in the tissue. The method is useful for increasing or decreasing hair follicle development, tooth development or sweat gland development, in a tissue of a patient suffering from an ectodermal disease such as X-linked hypohidrotic ectodermal dysplasia (XLHED), autosomal recessive hypohidrotic ectodermal dysplasia (HED) or alopecia. The method is useful for decreasing hair follicle development in a subject suffering from hirsutism. The method is also useful for treating breast cancer and ectopic teeth, burns and trauma of skin due to mangery. The present sequence represents the amino acid sequence of mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 YFIYSQVEVYYINFTDFASYEVVVDEKPFLQCTRSIBTGKTNYNTCYTAGVCLLKARQKI 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MGYPEVERREPLPAAAPRERGSGGCGCRGAPARAGEGNSCRLFLGFFGLSLALHLITLCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGGPNGPPGPPGPPGPPGPPG1PG1PG1PG1PGTTVMGPPGPPGPPGPGPPGPQGPPGLQGPSGAADK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----EVYYINFTDFASYEVVVDEKPFLQCTRSIETGKTNYNTCYTAGVCLLKARQKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                              89.3%; Score 1873; DB 7; Length 377; 90.8%; Pred. No. 1.9e-137; ive 2; Mismatches 20; Indels 1
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/note= "linker peptide"
266. .412
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Best Local Similarity 90.8
Matches 355; Conservative
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/note=
                                                                                                                                                                                                                                                                                                                                                      Sequence 377 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sebaceous gland.
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This invention describes a novel recombinant fusion protein which comprises an immunoglobulin Fc segment, the extracellular region of a cumour necrosis factor (TNF) and optionally a transition region, including a linker. The TNF ligands used in the method include Fash, TNF-calpha or TNF-gamma, TRAIL or most preferred, EDAI or 2. The Fc fragment of an including the hinge region and domains CH2 and CH3 of the Fc segment of an igG, particularly human. The linker optionally includes a protease cleavage site. The N-terminus of construct may have a signal sequence, or cleavage site. The N-terminus of construct may have a signal sequence, secretory signal sequence and/or tag (e.g. Flag or His). The products of the invention have dermatological and depilatory activity. The construct, or other therapeutic agents, are administered parenterally (especially intravenously or intra-arterially) during pregnancy, especially as early intravenously or intra-arterially, during pregnancy, especially as early intravenously or intra-arterially, during pregnancy, especially or intra-arterially during pregnancy, especially as early at least 14 days. Nucleic acid encoding the construct, related vectors construct fusional deficiency with hyper IgM) and also alopaecia, hirsutism and inadequate functioning of the sweat and sebaceous glands. The fusion protein construct is soluble but etill retains ability to minic the physiological effects of TNF ligand. This sequence represents the fusion construct Fc-EDAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            296 SRITMNPKVFKLHPRSGELEVLVDGTYFIXSQVEVYXINFTDFASYBVVVDEKPFLQCTR 355
                                                                                                                                                                                                                                                                                                                                                                             New recombinant fusion protein, useful for treating deficiency of tumor necrosis factor ligand, particularly ectodermal dysplasia, comprises the ligand and immunoglobulin fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIETGKTNYNTCYTAGVCLLKARQKIAVKMVHADISINMSKHTTFFGAIRLGEAPAS 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 GKRSPOPOPKPOPKP---BPEGSLQ---VDENOPAVVHLQGGGSAIQVKNDLSGGVLNDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      215 GPPGPPGPPGPQGPPGLQGPSGAADKAGTRENQPAVVHLQGQGSAIQVKNDLSGGVLNDW
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Pred. No. 3.8e-52;
1; Mismatches 15; Indels
                                                                                                                                                                                                                                                                      Tschopp
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87.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 8; Fig D; 22pp; German.
                                                                                                                                 11-FEB-2002; 2002DE-01005583
                                                                                                                                                                              10-FEB-2002; 2002DE-01005368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 87.6°
Matches 155, Conservative
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                                                                                                                                                                                                                                                                      Schneider
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                                                                                                                                                                                                                         (APOX-) APOXIS SA
                                                                                                                                                                                                                                                                                                                                     N-PSDB; ADP75163
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                                               DE10205583-A1
                                                                                    21-AUG-2003
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ID ADP75
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AC ADP75
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DT 12-AU
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This invention describes a novel recombinant fusion protein which comprises an immunoglobulin Fc segment, the extracellular region of a tumour necrosis factor (TNP) and optionally a transition region.

C uncluding a linker. The TWP ligands used in the method include Fast, TNP-c including a linker. The TWP ligands used in the method include Fast, TNP-c alpha or TNP-gamma, TRAIL or most preferred, EDA1 or 2. The Fc fragment of contains the hinge region and domains CH2 and CH3 of the Fc segment of an entry particularly human. The linker optionally includes a protease cief, particularly human. The linker optionally includes a signal sequence, cleavage site. The N-terminus of construct may have a signal sequence, cleavage site. The N-terminus of construct may have a signal sequence, or other therapeutic agents, are administered parenterally (sepecially or intra-arterially) during pregnancy, especially as early intravenously or intra-arterially) during pregnancy, especially as early intravenously or intra-arterially) during pregnancy, especially as early car possible, e.g. for humans, in the first 3 months, every second day for at least 14 days. Nucleic acid encoding the construct, related vectors at least 14 days. Nucleic acid encoding the construct, related vectors cand transfected host cells, are useful in gene/cellular therapy of particularly ectodermal dysplasia (specifically the X-linked hypohydrotic form or X-linked immune deficiency with hyper IgM) and also alopaecia, form or X-linked immune deficiency with hyper IgM) and also alopaecia, form or X-linked immune deficiency with hyper IgM) and esbaccous glands. The fusion protein construct is soluble but still retains ability to mimic the physiological effects of TNF ligand. This sequence represents
                                     fusion protein; immunoglobulin; Fc region; TNF; tumour necrosis factor; FaBL; TNF-alpha; TNF-gamma; TRAIL; EDA1; EDA2; dermatological; depilatory; gene therapy; cellular therapy; ectodermal dysplasia; x-linked immune deficiency; hyper IgM; alopaecia; hirsutism; sweat gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New recombinant fusion protein, useful for treating deficiency of tumor necrosis factor ligand, particularly ectodermal dysplasia, comprises the ligand and immunoglobulin fragment.
                                                                                                                                                                                                                                                                                                                      /note= "higgl Fc aa248-473 of gi2765420"
                                                                                                                                                                                                                                                                                                                                                                                                             /note= "hEDA2 aa245-389"
Pusion construct ps1236 Fc:EDA2 protein.
                                                                                                                                                                                                                                                                                                                                                            /note= "linker peptide"
266. .410
                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                              "HA signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tschopp J;
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                                                                                                                                                                                                                                                                                   /note=
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                                                                                                                                     sebaceous gland
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                                                                                                                                                                               Homo sapiens.
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                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                               Peptide
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anhidrotic ectodermal dysplasia (EDA) gene. The gene has been mapped to the region Xq12-q13 by genetic linkage analysis and has been shown to contain a 200 kb intron inserted in the 3' end of the coding sequence. Deficiencies in the gene are observed by translocations with a breakpoint in the transcribed CpG island 3 at the Xq12-q13 locus. The EDA gene can be used to study the dynamics of EDA gene expression during foetal development, and processes affecting normal hair growth in adults. The EDA gene can also be used to study hair, sweat gland and tooth formation and growth, and ectodermal dysplasias
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
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242 GKRSPQPRPPRPQPKP---EPEGSLQ---VDENQPAVVHLQGGGSAIQVKNDLSGGVLNDW 295
                          SRITMAPKVFKLHPRSGELEVLVDGTYFIYSQVEVYYINFTDFASYEVVVDEKPFLQCTR 334
                                                                                                                                                                                                                                                                                     Human; anhidrotic ectodermal dysplasia; X chromosome; genetic linkage;
translocation; CpG island; foetal development; hair; sweat gland; tooth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 YLELRSELRRERGAESRIGGSGTPGTSGTLSSLGGLDPDSPITSHIGQPSFKQQPLEPGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MGYPBVERRELLPAAAPRERGSQGCGCGGAPARAGEGNSCLLFLGFFGLSLALHLLTLCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human anhidrotic ectodermal dysplasia gene - useful for research into
                                                                               SIETGKINYNTCYTAGVCLLKARQKIAVKMYHADISINMSKHTTFFGAIRLGEAPAS 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.4%; Score 700; DB 2; Length 135; 100.0%; Pred. No. 1.5e-46; Indels tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                Human anhidrotic ectodermal dysplasia protein.
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                                                                                                                                                                                  AAW44764 standard; protein; 135 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, Fig 7; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                    96US-00684672.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAV05851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-APR-1993;
                                                                                                                                                                                                                                                                                                                                         Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                      22-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hair growth.
                                                                                                                                                                                                                                           01-JUN-1998
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36.2%; Score 759; DB 7; Length 410; larity 86.4%; Pred. No. 1.4e-50; Conservative 1; Mismatches 15; Indels

Query Match Best Local Similarity Matches 153; Conserv

Sequence 410 AA;

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8; Gaps

166 GPPGAPGPPGPPGPPGLPGPKGDRGDAGPKGADGSPGPAGPVGSPGAPGPPGPP 225

189 GPPGPPGPQGPPGIPGIPGTT-

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AAW57646 standard; peptide; 357

AAW57646 RESULT

(first entry)

27-AUG-1998

AAW57646;

Collagen-like polymer

Collagen-like polymer; synthetic polymer; fibre coating; prosthetic device; catalytic substance.

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Novel DNA sequence encodes a polymer comprising segments of repeating units of 3-9 amino acids from natural collagen, i.e. the present intervening sequence contg. Collagen like protein (CLD)-CB, able to assemble into aligned structures formable into articles. The polymer comprises at least 2 segments joined by an unaligned intervening oligopeptide, other than the repeating unit. The polymer can be used to make fibres, films, membranes, emulaions, coatings, etc., useful as, e.g. specific binding materials, catalysts, purificin. agents, composites, laminates, adhesives, call growth surfaces, affinity columns and supports for biological materials. Typical applications include wound dressings, and in vivo prothesses. The polymer produces articles with good mechanical properties, and the intervening oligopeptide can provide a ligand for binding a mol., antibody, etc., or a chemically reactive site for coupling to proteins, etc.. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding protein contg. repeated fibroin derived segments - linked by oligopeptide with cell adhesion properties useful, e.g. in wound
                                                                                                                                                                                                                                                     Polymer; repeat unit; natural collagen; intervening oligopeptide; fibre; film; membrane; emulsion; coating; collagen like protein; pepodific blinding material; catalyst; purification agent; composite; laminate; adhesive; cell growth surface; affinity column; biological material support; wound dressing; in vivo prothesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.0%; Score 294; DB 2; Length 357; 32.4%; Pred. No. 2e-14; tive 9; Mismatches 71; Indels 6
                                                                                                                                                                                                                      Intervening sequence contg. collagen like protein (CLP)-CB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Col 101-104; 71pp; English.
                                                                                            AAR95115 standard; protein; 357 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86US-00927258.
87US-00114618.
88US-00269429.
89WO-US005016.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90US-00609716
                                                                                                                                                                                     (first entry)
121 AALHSDSQDGHQ 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cappello J, Ferrari FA;
                                                                                                                                                                    (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-238772/24.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 357 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-NOV-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-NOV-1989;
                                                                                                                                                                    25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                               US5514581-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-NOV-1986
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09-NOV-1988
                                                                                                                                                                                   03-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                               AAR95115;
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(PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

Ferrari FA, Cappello J;

WPI; 1998-387004/33.

91US-00791960. 92US-00972032. 95US-00577046.

86US-00927258. 87US-00114618. 88US-00269429. 90US-00609716.

96US-00642255

02-MAY-1996;

30-JUN-1998

04-NOV-1986; 29-OCT-1987 06-NOV-1990; 12-NOV-1991; 05-NOV-1992; 22-DEC-1995;

US5773249-A.

Synthetic.

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This sequence represents a unnatural collagen-like polymer of the invention. The products may be used as films, fibres, moulded objects and admixed with other natural or synthetic polymers or coatings on fibres, films, labware or other surfaces, e.g. prosthetic devices. The polymers films, labware or other surfaces, e.g. prosthetic devices. The polymers catalytic substances (where the amino acid sequence may specifically chelate a wide variety of elements), as purification media, composites, laminates or adhesives. They may also be combined with inorganic or organic materials such as carbon fibres, nylon fibres, nitrocellulose, etc., as flask coatings or in synthetic matrices for the growth and study of cells, as affinity columns or as supports for biological materials. The polymers have collagen-like properties, but may be easily expressed in micro-organisms in high efficiency. The new sequences can be tailored
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 ERGAESRIGGSGTPGTSGTLSSLGGLDPDSP--ITSHLGQPSPKQQPLEPGBAALHSDSQ 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant collagen-like polymers - useful for making gels, films,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
14.0%; Score 294; DB 2; Length 357;
Best Local Similarity 32.4%; Pred. No. 2e-14;
Matches 69; Conservative 9; Mismatches 71; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 357 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fibres, etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 DGHQMALLINFFFPDEKPYSEESRRVRRNKRSKSNEGADGPVKNKKKGKKAGPPGPNGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64;
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69; Conservative

Matches

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This invention relates to DNA encoding a proteinaceous polymer. The polymer comprises strands of repeating units of a natural protein capable of assembling into aligned structures, with at least 2 strands joined by an intervening oligopeptide other than the repeating units. The intervening oligopeptide is unaligned and the polymer has individual strands of the same or different repeating units. The DNA is useful for producing high molecular weight polymers of amino acids based on biologically and chemically active structural polymers. These polymers may be used to provide a variety of structures for different purposes, and to produce articles including coatings, or other (non)structural components, e.g. fibres, films, membranes, adhesives or emulsions, or with other compounds and/or compositions to form composites or imminates. Peptide sequences AAB63971-B63991 represent monomer sequences which can be used in the polymers of the invention. Oligonucleotide sequences AAB63370- AAP23370 and amino acid sequences AAB64002 are used in the construction of SLP and PCB-SLP polymers. Oligonucleotide sequences CC sequences AAB64008 are used in the construction of CLP (collagen like protein) polymers. Oligonucleotide sequences AAB64008 are used in the construction of CLP (collagen like protein) sequences AAB64008 are used in the construction of CLP (collagen like protein) sequences AAB64008 are used in the construction of CLP (collagen like protein) sequences AAB64008 are used in the construction of CLP (collagen like protein) sequences AAB64008 are used in the construction of Karain sequences AAB64008 are used in the construction of keratin sequences AAB64008 are used in the cust used in the construction of keratin
                                                 DGHQMALLNFFFPDEKPYSEEESRRVRRNKRSKSNEGADGPVKNKKKGKKAGPPGPNGPP 188
                                                                                                                                       .---- 212
                                                                                                                                                                                 166 GPPGAPGPPGPPGPPGPPGLPGPKGDRGDAGPKGADGSPGPAGPVGSPGAPGPPGPP 225
71 DRGDAGPKGADGSPGPAGPVGSPGAPGPPGPPGPPGAPGPPGPPGPPGPPGPPGLPGPKG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New DNA encoding a polymer with strands of repeating units of natural protein joined by intervening oligopeptide for producing high molecular weight polymers of amino acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proteinaceous polymer; repeat unit; structural polymer; coating; film; fibre; membrane; adhesive; emulsion; laminate; keratin; collagen.
                                                                          213 -VMGPPGPPGPPGPQGPPGLOGPSGAADKAGTR 244
                                                                                                                                                                                                                                                       226 GPPGAPGPPGPPGPPGLPGPKGDRGDAGPK 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
                                                                                                                                       189 GPPGPPGPPGIPGIPGIPGTT-----
                                                                                                                                                                                                                                                                                                                                                                                        AAB64008 standard; protein; 357 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLP-CB protein sequence SEQ ID 66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Col 41; 73pp; English.
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87US-00114618.
88US-00269429.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-OCT-1987;
09-NOV-1988;
06-NOV-1990;
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                                                 129
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71 ERGAESRIGGSGTPGTSGTLSSLGGLDPDSP--ITSHLGQPSPKQQPLEPGEAALHSDSQ 128
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                                                                                                                                                                                                                                                                                               131 D-------kgDAGPKGADGSPGPVGSPGAPGAPGPVGSPGAPGPPGPPGPP 165
                                                                                                                                                                                                                                                                                                                                        ----- 212
                                                                                                                                                                                                                                                                                                                                                                             166 GPPGAPGPPGPPGPPGPPGPPGDRGDAGPKGADGSPGPAGPVGSPGAPGPPGPP 225
                                                                                                                                                                                                                                                          129 DGHQMALLINFFFPDEKPYSEEESRRVRRNKRSKSNEGADGPVKNKKKGKKAGPPGPNGPP
                                                                                                                                            Gaps
polymers. Proteins and peptides represented by sequences AAB64015 AAB64049 are examples of polymers of the invention
                                                                                                                                          64;
                                                                                                       4; Length 357;
                                                                                                                                          71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            226 GPPGAPGPPGPPGPPGLPGPKGDRGDAGPK 258
                                                                                                                                                                                                                                                                                                                                                                                                                         213 -VMGPPGPPGPPGPQGPPGLQGPSGAADKAGTR 244
                                                                                                   Score 294; DB 4;
Pred. No. 2e-14;
9; Mismatches 7
                                                                                                                                                                                                                                                                                                                                            189 GPPGPPGPPGIPGIPGIPGTT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          completed: January 13, 2006, 16:13:31
                                                                                                   Query Match
Best Local Similarity 32.4%;
Matches 69; Conservative 9
                                                                Sequence 357 AA;
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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- protein search, using sw model OM protein January 13, 2006, 16:08:46; Search time 16 Seconds (without alignments) 2351.297 Million cell updates/sec Run on:

US-09-729-658C-2 2098 Title: Perfect score: Sequence:

1 MGYPEVERRELLPAAPRER..........NMSKHTTFFGAIRLGEAPAS 391

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched: 283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:* pir2:* pir3:* PIR 80:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		dР				
Result No.	Score	Query Match	Query Match Length	DB	ID	ij
-	280.5	13.4	1838	-	CGHU1V	
7	277	13.2	1464	7	S59856	collagen alpha 1(I
m	275.5	13.1	1433	7	A46053	bullous pemphigoid
4	275	13.1	1049		CGB07S	collagen alpha 1(I
ស	273.5	•	1843	~	S18803	collagen alpha 1(V
v	273	13.0	1532	~	A61262	collagen alpha 1(X
7	268.5	12.8	742	7	JC7595	scavenger receptor
æ	267.5	12.8	316	~	T20497	
σ	267	12.7		~	I50694	
10	267	12.7		~	A56101	collagen alpha 1(X
11	267	. 12.7		~	B56101	
17	266	12.7		Н	CGB01S	
13	265.5	12.7	-	Н	CGHU1S	
14	265	12.6		7	S16366	collagen alpha 2(I
15	264	12.6		-	CGHU1B	
16	263.5	12.6	1146	~	A38587	
17	263.5	12.6		~	A41182	collagen alpha 1(I
18	263.5	12.6	1487	~	B41182	
19	263	12.5		Н	CGHU2S	
20	260.5	12.4		~	820819	
21	259.5	12.4	302	7	T15936	
22	259.5	12.4		7	823297	
23	258.5	12.3		Н	A43291	
24	258	12.3	674	~	S13301	
25	258	12.3	680	Н	CGHU1D	alpha
56	258	12.3	1142	7	JX0369	
27	257.5	12.3	312	~	T25048	
28	257.5	12.3	1453	7	S21626	alp
59	256.5	12.2	688	~	A53330	

collagen alpha 1(I collagen alpha 1(I collagen alpha 3(I	collagen alpha 2(I collagen alpha 2(I collagen alpha 1(V collagen alpha 1(X	collagen alpha 1(x collagen alpha 1(1 collagen alpha 1(X hypothetical prote	hypothetical prote ORF2 protein - sai collagen alpha 3(I collagen alpha 1(X
CGHU6C CGHU7L CGHU3B	CGCH2S S23809 S15435 A53317	A53019 CGCH1S CGHU1B T21314	T32783 B34770 A39024 B40983
-	4444	90440	0000
1487 1466 1670	964 1414 744 1388	1418 684 1042 1806 301	329 102 471 633
12.2 12.2 12.1	11110	12.0	11.9
256.5 256 254	253.5 253.5 253.5 252.5	251.5 251.5 251 251 250.5	250.5 250 250 250
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ALIGNMENTS

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		(V) chain precursor -	
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		1 (V)	
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RESULT 1
CGHUIV
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COCHUIV

COCHUIV

N/Alternate names: procollagen alpha 1(V) chain
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence revision 03-Oct-1995 #text_change 09-Jul-2004
C;Accession: S18802; S16024; Ä61142; Name 130378; S43642; S58665
R;Greenspan, D.S.; Cheng, W.; Hoffman, G.G.
A;Greenspan, D.S.; Cheng, W.; Hoffman, G.G.
A;Title: The pro-alpha1(V) collagen chain. Complete primary structure, distribution of A;Reference number: S18802; MUID:9210S142; PMID:1722213

A,Molecule type: mRNA A,Rebidues: 1-1838 -CRES-A,Ecredues: 1-1838 -CRES-A,Cross-references: UNIPROT:Q15094; UNIPARC:UPI00006E982; GB:M76729; NID:g189519; PIDN B,Takahara, K.; Sato, Y.; Okazawa, K.; Okamoto, N.; Noda, A.; Yaoi, Y.; Kato, I. B,Takahara, K.; Sato, Y.; Okazawa, K.; Okamoto, N.; Noda, A.; Yaoi, Y.; Kato, I. A,Title: Chem. 266, 13124-13129, 1991 A,Title: Complete primary structure of human collagen alpha-1(V) chain. A,Reference number: S16024; MUID:91302336; PMID:2071595

A; Molecule type: mRNA A; Mote: parts of this sequence were determined by protein sequencing A; Note: parts of this sequence were determined by protein sequencing B; Mote: parts of this sequence were determined by protein sequencing A; Note: parts of this sequence were determined by protein sequencing B; Mote: parts of this sequence were determined by protein sequencing A; Note: parts of this sequence were determined by protein sequencing A; Title: Insulin binds to type V collagen with retention of mitogenic activity. A; Meserchence: under: A61142 A; Molecule type: protein A; Molecule type: protein A; Meserchences: UNIPARC: UPP10000173BB7 A; Note: the residue designated 'X' is probably glycosylated hydroxylysine; this cyanoge B; Yaoi, Y; Hashimoto, K; Koteabsshi, H; Takahara, K; Ito, M.; Kato, I. Biochim. Biophys: Acta 1035, 139-145, 1990 A; Title: Primary structure of the heparin-binding site of type V collagen. A; Reference number: S11303; MUID:90366601; PMID:2203476

A; Accession: S11303

A; Molecule type: protein
A; Residues: 823-824, 'X', 826-848,'I', 850-851,'P', 853,'PR', 856-893,'D', 895-932,'X', 934-95
A; Cross-references: UNIPARC:UPI0000173BB8
A; Note: the residues designated 'X' are probably glycosylated hydroxylysine; this seque R; Seyer, J.M.; Kang, A.H.
Arch. Biochem. Blophys. 271, 120-129, 1989
A; Title: Covalent structure of collagen: amino acid sequence of three cyanogen bromide-A; Reference number: 803978; MUID:89227189; PMID:2496661

A; Molecule type: protein

A;Cross-references: UNIPARC:UP10000173BB9 A;Note: there are a number of inconsistencies between the sequences in figures 6 and 7;

A; Residues: 621-640, 'G', 642-649,'L', 651-662,'B', 664-667,'Q', 669-676,'Q', 678-683,'P', 685

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357 PLGPPGEKGKLGVPGLPGYPGRQGPKGS----IGFPGFP--
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ilarity 31.8%;
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A,MSP position: 9434-2944-3
C,Complex: type V collagen may be a homotrimer of alpha 1(V) chains, a heterotrimer of talpha 2(V) chain sq44-2944-3
C,Complex: type V collagen may be a homotrimer of alpha 1(V) chains, a heterotrimer of talpha 2(V) chain and one alpha 3(V) chain, initially linked by disulfide bonds among the ength, is formed with desmosine cross-links made from lysine and allysine residues of Function: a formed with desmosine cross-links made from lysine and allysine residues of Function: a formed with desmosine cross-links made from lysine and allysine residues of Function: a formed with desmosine cross-links made from lysine and allysine residues of Function: a formed with desmosine among the collagen alpha 1(V) chain, size a formed collagen alpha 1(V) chain, size a formed callagen alpha 1(V) chain, size a formed callagen alpha 1(V) chain, short form #status predicted F;53-157/Region: carboxyl-terminal propeptide #status predicted callagen alpha 1(V) chain, short form #status predicted F;53-157-1605/Region: carboxyl-terminal propeptide #status predicted callagen alpha 1(V) chain short form) carboxyl-terminal propeptide #status predicted callagen alpha 1(V) callagen V carboxyl-terminal propeptide carboxyl-terminal propeptide carboxyl-terminal propeptide carboxyl-terminal propeptide carboxyl-terminal carboxyl-terminal propeptide carboxyl-terminal c
R; Moradi-Ameli, M.; Rousseau, J.C.; Kleman, J.P.; Champliaud, M.F.; Boutillon, M.M.; Ber Eur. J Blochem. 221, 987-995, 1934

A; Title: Diversity in the processing events at the N-terminus of type-V collagen. A; Reference number: 843642; MUID:9423164; PMID:8181482

A; Accession: 843642; MUID:9423164; PMID:8181482

A; Accession: 843642; MUID:9423164; PMID:8181482

A; Accession: 843642; MUID:9423164; PMID:818188

A; Residues: 565-576; 756-758, 7x', 760-763, 7x', 765-772; 1012-1029; 1219-1232; 1465-1474, 7x', 14

A; Residues: 565-576; 756-758, 7x', 760-763, 7x', 765-772; 1012-1029; 1219-1232; 1465-1474, 7x', 14

A; Residues: 565-576; 756-758, 7x', 760-763, 7x', 765-772; 1012-1029; 1219-1232; 1465-1474, 7x', 14

A; Residues: Li.; Broah, S.; Chapin, S.; Fessler, J.H.

J. Biol. Chem. 261, 5034-5040, 1986

A; Title: Tyrosine sulfaction in precursors of collagen V.

A; Reference number: A56977; MUID:8616826; PMID:3082875

A; Title: Transcriptional promoter of tyrosine sulfate in the amino-terminal propept R; Lee, S.; Greenspan, D.S.

B; A; Recension: S18665; MUID:95374437; PMID:7646438

A; Recension: S18665; MUID:95374437; PMID:7646438

A; Residues: preliminary; not compared with conceptual translation

A; Residues: 1-36 cLEE>

A; Cross-references: UNPPARC:UPI000007363D; GB:L38808; NID:91020325; PIDM:AA79853.1; PIC

C; Coment: Pollines and Uyaines at the third position of the tripeptide repeating unit (are 5-hydroxylated and subsequently 0-glycosylated.

C; Coment: Pollines and Uyaines at the third position of the hererotrimers are probably processed to the long form.

C; Coment: A long form of the mature protein containing part of the amino-terminal proper C; Comment: A long form of the mature protein containing part of the amino-terminal proper C; Genetics:

C; Comment: A long form of the mature protein containing part of the amino-terminal proper C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
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9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 83
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71

13 PAAAPRERGSOGC-GCGGAPARAGEGNSCLLFLGFFGLSLALHLLTLCCYLELRSELRRE

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A; Introns. 29/1; 95/3; 112/3; 150/3; 175/3; 193/3; 211/3; 229/3; 247/3; 265/3; 283/3; 25 88/3; 673/3; 706/3; 776/3; 778/3; 796/3; 814/3; 850/3; 868/3; 886/3; 940/3; 976/3 68/3; 673/3; 706/3; 778/3; 778/3; 796/3; 814/3; 850/3; 868/3; 886/3; 976/3; 976/3 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 678/2; 
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A;Residues: 1442-1464 <MET>
A;Cross-references: UNIPARC:UPI000016CCAB; EMBL:X57983; NID:950476; PIDN:CAA41048.1; PIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complete DNA
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A; Reference number: $62120

A; Accession: $62120

A; Molecule type: DNA

A; Molecule type: DNA

A; Cross-references: UNIPARC: UD10000029506; EMBL: XE2046; NID: 9575321; PIDN: CAA36279.1; I

A; Cross-references: UNIPARC: D10000029506; EMBL: XE2046; NID: 9575321; PIDN: CAA36279.1; I

Biochim. Biophys. Acta 1089, 241-243, 1991

A; Title: Specific hybridization probes for mouse type I, II, III and IX collagen mRNAB

A; Reference number: $16176; MUID: 91274355; PMID: 2054384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          955 GPTGFPGPKGPPGPPGKDGLPGHPGQRGETGPQGKTGPPGPPGVVGPQGPTGETGPMGER 1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RRERGAESRIGGSGTPGTSGTLSSIGGLDPDSP--ITSHIGQPSPKQQPLEPGEAALHSD 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   872
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                                                                                                                                                                                                                                                                                                                                      ------PRGERGPRGITGKPGPKGNSGGDGP-----AGPPGERGPNGPQ 954
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RGAESRIGGSGTPGTSGTLSSLGGLDPDSPITSHLGQPSPKQQPLEPGEAALHSDSQDGH 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               collagen alpha 1(III) chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: S59856; S62120; S16773
R;Toman, P.D.; de Crombrugghe, B.
Gene 147, 161-168, 1994
A;Ritle: The mouse type-III procollagen-encoding gene: genomic cloning and A;Ritle: The mouse: S59856; MuID:95011609; PMID:7926795
A,Rocession: S59856
A,Molecule type: DNA
A;Residues: 1-1464 <TON>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Readude: 1-1464 <TOM>
A; Cross-references: UNIPROT: P08121; UNIPARC: UPI0000177386; EMBL: X52046
R; Toman, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82;
                                                                                                                                                                                                                               OMALLINFFPPDEKPYSEEESRRVRRNKRSKSNEGADGPVKNKKKGKKAGPP-
                                                                                                                             -----GKPGPRGQRGPTG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        -TTVMGPPGPPGP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GHPGPPGPPGEQGLPGLAGKEGTK-GDPGPAGLPGK 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -- PGPOGPPGLOGPSGAADKAGTRENOPAVVHLQGQ 256
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Pred. No. 2.2e-10;
5; Mismatches 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRGGPGERGEHGPPGPAGFPGAPGQNGEPGA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPPGPPGPQGPPGIPGIPG-
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collagen. II. The amino acid seque

Beq.

The amino acid

collagen. III.

collagen. V. The amino acid seque-

VI. The amino acid segu

collagen.

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A,Molecule type: protein
A,Residues: 423-571 cBEN>
A,Cross-references: UNIPARC:UP10000173B8C
A,Cross-references: UNIPARC:UP10000173B8C
A,Elang, H.; Glanville, R.W.; Fietzek, P.P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 841-850, 1979
A,Title: The covalent structure of calf skin type III collagen. IV. The amino acid sequence number: A38003; MUID:80026029; PMID:488909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Residues: 87-106;1017-1029;1037-1049 < HEN>
A; Residues: 87-106;1017-1029;1037-1049 < HEN>
A; Residues: 87-106;1017-1029;1037-1049 < HEN>
A; Cross-references: UNIPARC:UPI0000173B90; UNIPARC:UPI0000173B91; UNIPARC:UPI0000173B92
C; Comment: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are C; Comment: The type III collagen molecule is a trimer of identical chains, linked to ea C; Superfamily: collagen alpha ilf; chain; fibrillar collagen carboxyl-terminal homology C; Reywords: collagen alpha ilfil chain #status experimental < CAB>
F;1-1049/Product: collagen alpha ilfil chain #status experimental < CAB>
F;1-14/Region: amino-terminal nonhelical telopeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochem. J. 318, 497-503, 1996
A;Title: Cross-link analysis of the C-telopeptide domain from type III collagen.
A;Reference number: S71946; MUID:96404897; PMID:8809038
A;Accession: S71946
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F;95,107,119,938,950/Modified site: 5-hydroxylysine (Lys) #status experimental
F;107,950/Modified site: allysine (Lys) #status predicted
F;107/Binding site: carbohydrate (Lys) (covalent) #status experimental
F;107/Binding site: carbohydrate (Lys) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accesion: A38005; MUD:8002601; A;Accesion: A38005; MUD:8005; PMID:80013B8E
A;Residues: 809-947 < DEW2>
A;Cross-references: UNIVERSITY & A;Cross-references: UNIVERSITY & A;Cross-references: UNIVERSITY & A;Accesion: A38005; MUD:80026031; PMID:488911
A;Accession: A38005
                                                                                                                                                                                                                                                             R;Bentz, H.; Fletzek, P.P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 833-840, 1979
A;Title: The covalent structure of calf skin type III c
A;Reference number: A38002; MUID:80025028; PMID:488908
A;Accession: A38002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ribewes, H.; Fietzek, P.P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 851-860, 1979
A;Title: The covalent structure of calf skin type III of
A;Reference number: A38004; MUID:80026030; PMID:488910
R;Dewes, H.; Fietzek, P.P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 821-832, 1979
A;Title: The covalent structure of calf skin type III (
A;Reference number: A38001; WUID:80026027; PMID:488907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (R-G-D) motif
(R-G-D) motif
(R-G-D) motif
(R-G-D) motif
(R-G-D) motif
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                                                                                                                                                                         A;Molecule type: protein
A;Residues: 243-422 <DEW1>
A;Cross-references: UNIPARC:UPI0000173B8B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Remiduem: 572-808 <LAN>
A;Crosm-referencem: UNIPARC:UPI0000173B8D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: protein
A;Residues: 948-1049 <ALL>
A;Cross-references: UNIPARC:UP10000173B8F
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P.587-589/Region: cell attachment
P.752-754/Region: cell attachment
P.875-877/Region: cell attachment
P.878-880/Region: cell attachment
P.935-937/Region: cell attachment
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llarity 31.3%;
Conservative !
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                                                                                                                                          A; Accession: A38001
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Best Local S
Matches 77
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C;Species of beer 1986 #sequence revision 04-Dec-1986 #text change 09-Jul-2004
C;Date: 04-Dec-1986 #sequence revision 04-Dec-1986 #text change 09-Jul-2004
C;Accession: A02862; A38001; A38002; A38004; A38004; A38005; S71946
C;Accession: A02862; A38001; A38002; A38004; A38005; S71946
Hoppe-Seyler's Z. Physiol. Chem. 360, 869-820, 1979
A;Title: The covalent structure of Calf Skin type III collagen. I. The amino acid sequent A;Reference number: A02862; MUID:80026026; PMID:488906
                                                                                                                                                                                                                                                                                                                                                                                                        Cipate: 21-Sep-1993 #sequence_revision 21-Sep-1993 #text_change 09-Jul-2004
Cipate: 21-Sep-1993 #sequence_revision 21-Sep-1993 #text_change 09-Jul-2004
Cipatesion: A46653
Tali, K.; Tamai, K.; Tan, E.M.L.; Uitto, J.
J. Biol. Chem. 266, 8825-8834, 1993
A;Title: Cloning of type XVII collagen. Complementary and genomic DNA sequences of mouse egment, and unusual features in the 5'-end of the gene and the 3'-untranslated region of A;Reference number: A46053; MUID:93232041; PMID:8473327
A;Accession: A46053
A;Accession: A46053
A;Actus: preliminary
A;Molecule type: mRNA
A;Residues: 1-1433 <LII>A;Residues: 1-1433 <LII>A;Accession: A5,Note: sequence extracted from NCBI backbone (NCBIN:129627, NCBIP:129628)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGPPGPKGDQGDPGVPGTPGISGGLSHGASSSTLYMQGPPGPPGPPGPPGSLSSSGQDIQ 1003
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             --GGRGLPGPPGN---NGNPGPPGPSG 896
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                                                                                                                                                                               897 APGKDGPPGPAGNSGSPGNPGIAGPKGDAGQPGEKGPPGAQGPPGSPGPLGIAGLTGAR 955
                                                                                                                                                                                                                                                                                                                                                                             C,Species: Mus musculus (house mouse)
C,Date: 21-Sep-1993 #sequence_revision 21-Sep-1993 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SELRRERGAESRIGGSGTPGTSGTLSSLGGL---DPDSPIT-----SHLGQPSPKQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLEPGEAALHSDSQDGHQMALLNFFPDBKPYSEEESRRVRRNKRSK--SNEGAD--GPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171 KNKKKGKKAGPPGPNGPPGP--PGPPGPQGPP--GIPGIPGIPG-----TTVMGPPGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247 OPAVVHLQGQGSAIQVKNDLSGGVLNDWSRITMNPKVFKLHPRSGBLEVLVDGTYFIYSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGPAGPAGL--PGQQG-----PRGEPGLAGDSFLSSGSSISEVLSAQGVDLRGP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                               187 PPGPPGPPGPPGIPGIPGIPGTT-VMGPPGPPGPPGPQGPPGLQGPSGAADKAGTR
                                                                                                                                                                                                                                                                                                                                           type XVII collagen alpha 1-chain -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   || | ::||:|
751 PAGADGQGSRGEQGLTGMPGTRGPPGPAGDPG------
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                                                                                                                                                                                                                                                                                                                   A46053
bullous pemphigoid antigen, BPAG2,
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Best Local Similarity 26.5'
Matches 99; Conservative
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6 96; 68, Indels Score 275; DB 1; Pred. No. 2.1e-10;

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A; Residues: 1-1532 errs.
A; Residues: 1-1532 errs.
A; Coss-references: UNIPROT: Q9UMD9; UNIPARC: UPI000006F673; GB: M91669; NID: g179516; PIDN: A; Cross-references: UNIPROT: Q9UMD9; UNIPARC: UPI00006F673; GB: M.G.; Chu, M.L.; Uitto, J. J. Biol. Chem. 266, 24064-24069, 1991
A; Title: Genomic organization of collagencus domains and chromosomal assignment of human A; Reference number: I55345; MUID: 92084712; PMID: 1748679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      scavenger receptor with C-type lectin type I - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
C;Accession: JC7595
R;Nakamura, K.; Punakoshi, H.; Miyamoto, K.; Tokunaga, F.; Nakamura, T.
Biochem. Biophys. Res. Commun. 280, 1028-1035, 2001
A;Title: Molecular cloning and functional characterization of a human scavenger receptor A;Reference number: JC7595; MUID:21092718; PMID:11162630
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C;Comment: This receptor, a member of the scavenger receptor family, belonging to the ty
important role in host defense. It forms a timer and plays a role in recognizing infect
                                                                                                                                                                                                                                                                                                       A; Modecule type: mRNA
A; Residues: 543-890, Pv <RE2>
A; Residues: 543-890, Pv <RE2>
A; Cross-references: UNIPARC:UP1000006F72A; GB:M63730; NID:g179520; PIDN:AAA51839.1; PID:
R; Gludica: G. J; Squiquera, H.L.; Elias, P.M.; Diaz, L.A.
J. Clin. Invest. 87, 734-738, 1991
A; Title: Identification of two collagen domains within the bullous pemphigoid autoantige
A; Reference number: A61262; MUID:91123476; PMID:1846881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 EAALHSDSODGHOMALLNFFFPDEKPYSEEESRRVRRNKRSKSNEGADGPVKNKKKGKKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 13.0%; Score 273; DB 2; Length 1532; Similarity 31.2%; Pred. No. 4.3e-10; 85; Conservative 13; Mismatches 64; Indels 11
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A,Map position: 18p11.32
C;Keywords: coiled coil; glycoprotein; transmembrane protein
              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA__
                                                                                                                                                                                                                                                    A;Accession: 155345
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: GDB:COL17A1; BPAG2; BP180
A;Cross-references: GDB:131396; OMIM:113811
A;Map position: 10q24.3-10q24.3
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Best Local Similarity
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A; Residues: 1-742 <NAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecule type: mRNA
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NyAlternate names: bullous pemphigoid 180K autoantigen BPAG2; bullous pemphigoid antigen
SySpecies applies (man)
C;Species: Homo saplens (man)
C;Date: 12-May-1994 #sequence revision 12-Jul-1996 #text_change 09-Jul-2004
C;Accession: 156325; 155345; A61262
R;Giudice, G.J.; Emery, D.J.; Dlaz, L.A.
J. Invest. Dermatol. 99, 243-250, 1992
A;Title: Cloning and primary structural analysis of the Bullous pemphigoid autoantigen,
A;Refarence number: 156325; MUID:92381323; PMID:1324962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
518803
collagen alpha 1(V) chain - hamster
C,Species: Cricetinae gen. sp. (hamster)
C,Species: Cricetinae gen. sp. (hamster)
C,Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 16-Dec-1998
C,Accession: 818803
**,Title: The pro-alpha1(V) collagen chain. Complete primary structure, distribution of e A,Title: The pro-alpha1(V) collagen chain. Complete primary structure, distribution of e A,Reference number: 818802; MuID:92105142; PMID:172213
A,Accession: 818803
A,Esterence number: 1-1843 cGRE>
A,Molecule type: mRNA
A,Residues: 1-1843 cGRE>
A,Cross-references: UNIPARC:UPI00001773AC
C,Superfamily: collagen alpha 1(V) chain; fibrillar collagen carboxyl-terminal homology
F;1620-1842/Domain: fibrillar collagen carboxyl-terminal homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         960 GPIGEPGPKGPPGEPGKDGLPGHPGQRGEIGFQGKTGPPGPPGVVGPQGPTGETGPMGER 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----AGPPGERGPNGITGKPGPKGNSGGDGP-----AGPPGERGPNGPQ 959
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                                                     RRERGAESRIGGSGTPGTSGTLSSLGGLDPDSPITSHLGQPSPKQQPLEPGEAALHSDSQ 128
                                                                                                                                                                      DGHQMALLINFFFPDEKPYSEEESRRVRRNKRSKSNEGADGPVKNKKKCKKAGPPGPNGPP 188
                                                                                                                                                                                                                                                                                                                                          735 GPPGSSGAPGKDGPPGPPGSNĆAPGSPGISGPKGDSGPPGERGAPGPQGPPGAPGPLGIA 794
                                                                                                                                                                                                                               71
                                                                                            RGAESRLGGSGTPGTSGTLSSLGGLDPDSP1TSHLGQPSPKQQPLEPGEAALHSDSQDGH
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                                                                                                                                                                                                                                                                                     GPP------GPPGPPGIPGIPGIPGIT-VMGPPGPPGPPGPPGLQGPSGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 PAAAPRERGSOGC-GCGGAPARAGEGNSCLLFLGFFGLSLALHLLTLCCYLELRSELRRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 1843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              862 PLGPTGEKGKLGVPGLPGYPGRQGPKGS----IGFPGFP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1020 GHPGPPGPPGEQGLPGVAGKEGTK-GDPGPAGLPGK 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.0%; Score 273.5; DB 2; 29.7%; Pred. No. 4.8e-10; iive 9; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223 --PGPQGPPGLQGPSGAADKAGTRENQPAVVHLQGQ 256
PRGGPGERGEQGPPGPAGFPGAPGQNGEPGA-
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nes 82; Conservative
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57 TLCCYLELRSELRRERGAESRLGGSGTPGTSGT-
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A;Experimental source: clone P02D10
C;Genetics:
F;1-39/Domain: cytosolic (amino-terminus) #status predicted <CYT>
F;16-19/Region: internalization signal YKRF
F;40-56/Domain: transmembrane #status predicted <TMM>
F;57-112/Domain: extracellular #status predicted <TMM>
F;57-112/Domain: extracellular #status predicted <CMC>
F;113-335/Domain: colled coil #status predicted <CMC>
F;113-335/Domain: serime/threonine-rich #status predicted
F;440-589/Domain: collagen-like #status predicted <CML>
F;607-732/Domain: C-type lectin/carbohydrate recognition domain #status predicted <CRD>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 GTPGTSGTLSSLGGLDPDSPITSHLGQPSPKQQPLEPGEAALHSDSQDGHQMALLNFFFP 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   483 ERGPIGPAGPPGERGGKGSK---GSQGPKGSRGSPGKPGPQGPSGDPGPPGPPGKEGLPG 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGPQGPPGIPGIPGIPGTTVMG---PPGPPGPPGPQGPPGLQGPSGAADKAGTRENQP 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein F02D10.1 - Caenorhabditis elegans C.Species: Caenorhabditis elegans C.Species: Caenorhabditis elegans C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C.Accession: T20497 #Swinburne, J. submitted to the EMBL Data Library, November 1995 A.Reference number: Z19283 A.Accession: T20497 #Shatus: preliminary; translated from GB/EMBL/DDBJ A.Status: preliminary; translated from GB/EMBL/DDBJ A.Residues: 1-316 - WML-A.Residues: A.Status: A.Stat
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collagen alpha 1(III) chain - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #Bequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: IS0694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142 DEKPYSEEESRRVRRNKRSKSNEGADGPVKNKKKKKRGPPGPPGPPGPPGPPGP-----PG
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                                                                                                                                                                                                                                                                                                                                                                37;
                                                                                                                                                                                                                                                                                            12.8%; Score 268.5; DB 2; Length 742; larity 37.2%; Pred. No. 4e-10; Conservative 13; Mismatches 63; Indels 37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 316;
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63;
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Pred. No. 1.9e-10;
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32.8%;
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Best Local Similarity
Matches 78; Conserv
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 67; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: CESP: F02D10.1
A; Map position: X
A; Introns: 56/3
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J. Biol. Chem. 269, 16443-16448, 1994
A.Title: An alternative transcript of the chick type III collagen gene that does not enc.
A.Accession: 150694
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Residues: 1-886 <NAH>
A.Residues: 1-886 <NAH>
A.Gross-references: UNIPROT:P12105; UNIPARC:UPI000017125A; EMBL:U07973; NID:g520454; PIDC; Genetics:
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C;Species Mus musculus (house mouse)
C;Date: 03-Oct-1995 #sequence revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: A56101; A58371; $72450; S65595
R;Rehn, M.; Pihlajaniemi, T.
B;Rehn, M.; Pihlajaniemi, T.
A;Title: Identification of three N-terminal ends of type XVIII collagen chains and tiss tif homologous to rat and Drosophila frizzled proteins.
A;Reference number: A56101; MUID:95181468; PMID:7876242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: AS8371
A; Accession: AS8371
A; Molecule type: mRNA
A; Reference number: 872450
A; Accession: 873450
A; Accession: 873450
A; Accession: 873450
A; Accession: 873450
A; Coss - references: UNIPARC:UP1000016CCB8; EMBL:L122545; NID:g348968; PIDN:AAA19787.1; P
A; Cross - references: UNIPARC:UP1000016CCB8; EMBL:L122545; NID:g348968; PIDN:AAA19787.1; P
A; Cross - references: UNIPARC:UP1000016CCB8; EMBL:L122545; NID:g348968; A: Osen, A.B.R.
B; Cross - Rain Acad. Sci. U.S.A. 91, 4229-4233, 1994
A; Title: Isolation and sequencing of CDNAs for proteins with multiple domains of Gly-Xa.
                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: COL3A1
C;Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology;
P;30-90/Domain: von Willebrand factor type C repeat homology <VWC>
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Proc. Natl. Acad. Sci. U.S.A. 91, 4234-4238, 1994
A;Title: Alphal(XVIII), a collagen chain with frequent interruptions in the collagenous A;Reference number: A58371; MUID:94240112; PMID:8183894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: A56101
A;Molecule type: mRNA
A;Residues: 1-103 <REH1>
A;Cross-references: UNIPROT:P39061; UNIPARC:UPI000016CAD0; GB:U11636; NID:g618427; PIDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PKGERGENGTPGARGPPGEEGKRGANGEPGONGVPGTPGERGS----PGPRGLPGS---- 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----LSSLGGLD--PDSPIT 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SHLGQPSPKQQPLEPGBAALHSDSQDGHQMALLNPPPDEKPYSEESRRVRRNKRSKSN 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----KGN 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGADGPVKNKKKGKKAGPPGPNGP-----PGPPGP-----PGPQGPPGIPGI 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 PEVERREL-LPAA--APRERGSQGC----GCGGAPARAGEGNSCLLFLGFFGLSLALHLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    collagen alpha l(XVIII) chain precursor, short splice form - mouse N_1Contains: endostatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.7%; Score 267; DB 2; Length 886; 32.5%; Pred. No. 6e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indela
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGGPGPAGENGKPGEPGPKGDIGGPGPPGPKGENGIPGERGPQ 685
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A;Molecule type: mRNA
A;Residues: 487-1146, L., 1148-1193, 'F',1195-1210,'R',1212-1512,'L',1514-1522,'F',1524-16
A;Cross-references: UNIPARC:UPIO00016CCB8; EMBL:L22545; NID:9348966; PION:AAA19787.1; PI
R;Oh, S.P.; Kamagata, Y.; Muragaki, Y.; Timmons, S.; Ooshima, A.; Olsen, A.B.R.
Proc. Neall Acad. Sci. U.S.A. 91, 4229-4233, 1994
A;Title: Isolation and sequencing of CDNAs for proteins with multiple domains of Gly-Xaa
A;Reference number: A58370; MUID:94240111; PMID:8183893
                                                                                                                                                                                   A;Cross-references: UNIPARC:UPI000017A14C; GB:U11637; NID:g618429
A;Experimental source: splice form clones PE8.1, PE19, PE15.2
R;Oh, S.P.; Kamagata, Y.; Muragaki, Y.; Timmons, S.; Ooshima, A.; Olsen, B.R.
submitted to the EMBL Data Library, August 1993
A;Reference number: S72450
              source: splice form clone PE17.24
                                                                                                        A; Molecule type: mRNA
A; Residues: 1-239, 487-562 <REH2>
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A; Reference number: A58370; WUID:94240111; PMID:8183893
A; Accession: 555595
A; Accession: 555595
A; Molecule type: mRN
A; Residues: 28-1315 cOHS-
A; Cross-references: UNIPARC: UNIPARC: UNIONO017A14D; EMBL:122545
A; Cross-references: UNIPARC: UN
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N;Contains: collagen alpha 1(XVIII) chain precursor, medium splice form; endostatin
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 03-Oct-1995 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: B56101; C56101; S72450; S65595; PN0675; A54072; A58816
R;Rehn, M.; Pihlajaniemi, T.
J; B101. Chem. 270, 4705-4711, 1995
A;Title: Identification of three N-terminal ends of type XVIII collagen chains and tissu tif homologous to rat and Drosophila frizzled proceins.
A;Reference number: A56101; MUID:95181468; PMID:7876242
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A, Rediducie type: mRNA
A, Rediducie: 1-562 «REHI.»
A, Cross-references: UNIPROT: Q61434; UNIPARC: UPI000016CAD1; GB: U11637; NID: g618429; PIDN:
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P;172-228/Disulfide bonds: #status predicted
P;1740,245,1257/Binding site: carbohydrate (Ser) (covalent) #status predicted
P;451,454,594/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 EPGEAALHSDSODGHOMALLNFFFPDEKPYSEEESRRVRRNKRSKSNEGADGPVKNKKKG 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----- PGPQGPPGIPGIP 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        420 PGIGPRGPPGPPGPPGPSFRQDKLTFIDMEGSGFSGDIESLRGPRGFPGPPGPPGPPGVPGLP 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           329 KGOKGEPGAQGPPGPAGPQGPAGPVVQSPNSQPVPGAQGPPGPPGPGGPPGKDGTPGRDGEPG 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GEPGRFGINGSYAPGPAGLPGVPGKEGPPGPPGPPGPPGKEGPPGVAGQKGS 534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 KKAGPPGPNGPPGPPGP-
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A; Molecule type: mRNA
A; Residues: 487-1512, 'L',1514-1522,'F',1524-1683,'V',1685-1774 <OH2>
A; Cross-references: UNIPARC:UPIO00017A14D; EMBL:L22545
R; Abe, N.; Muragaki, Y.; Yoshloka, H.; Inoue, H.; Ninomiya, Y.
B; Cchem. Biophys Res. Commun. 196, 576-582, 1993
A; Title: Identification of a novel collagen chain represented by extensive interruptions
A; Reference number: PN0675; MUID:94059075; PMID:8240330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 635-1774 <ABE>
A;Cross-references: UNIPARC:UP100000B7D60
R;Rehn, M.; Hintikka, E.; Pihlajaniemi, T.
J Biol. Chem. 269, 13929-13935, 1994
A;Title: Primary structure of the alphal chain of mouse type XVIII collagen, partial str
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA; mRNA
A; Residues: 1293-1403, 'R',1405-1774 <REH3>
A; Cross-references: UNIPARC: UP1000016CAAB; GB: U03714; NID: 9487733; PIDN: AAA20657.1; PID:
KFO Kellly, M.S.; Boehm, T.; Shing, Y.; Fukai, N.; Vasios, G.; Lane, W.S.; Flynn, E.; Bi
Cell 88, 277-285, 1997
A; Title: Endostatin: an endogenous inhibitor of angiogenesis and tumor growth.
A; Reference number: A58816; MUID: 97160848; PMID: 9008168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lated and subsequently O-glycosylated.
C.Comment: The different splice forms of collagen alpha 1(XVIII) may be involved in peri
C.Comment: Endostatin is released from collagen alpha 1(XVIII) chain by the action of un
ay be useful in treating solid tumors.
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A; Map position: 10:41.0
A; Amap positi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Experimental source: hemangioendothelium cells
A,Note: inhibits endothelial cell proliferation
C,Comment: Prolines and lysines at the third position of the tripeptide repeating unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Reference number: A54072; MUID: 94245707; PMID: 8188673
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A,Residues: 1591-1610 <ORE>
A,Cross-references: UNIPARC:UP10000499D2
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A; Accession: A43048
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A;Title: The covalent structure of collagen. 2. The amino-acid sequence of alphal-CB7
A;Reference number: A91211; MUID:74086118; PMID:4359390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Collagen alpha 1(I) chain - bovine (tentative sequence) (fragments)
C;Species: Bos primigenius taurus (cattle)
C;Becies: 24-Apr-1984 #sequence revision 31-Dec-1993 #text change 09-Jul-2004
C;Date: 24-Apr-1984 #sequence revision 31-Dec-1993 #text change 09-Jul-2004
C;Accession: A91193; A91229; A9131; A91211; A91201; A91200; A43048; A02853
R;Rauterberg, J.; Timpl, R.; Futchmayr, H.
Eur. J. Biochem. 27, 231-337, 1972
Bur. J. Biochem. 27, 231-337, 1972
A;Atitle: Structural characterization of N-terminal antigenic determinants in calf and la,Accession: A91193; MUID:72255334; PMID:4115172
F;1442-1459/Domain: collagenous #status predicted <CO10>
F;1591-1774/Product: endostatin #status predicted <EST>
F;1598-1774/Region: multiplexin collagen carboxyl-terminal homologous
F;1534,361,947/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;699,704,1716/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;910,913,1053/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                    72 RGAESRIGGSGTPGTSGTLSSLGGL--DPDS-PITSHLGQPSPK-------QQPL 116
                                                                                                                                                                                                                                                                                                                 788 KGQKGEPGAQGPPGPAGPQGPAGPVVQSPNSQPVPGAQGPPGPQGPPGKDGTPGRDGEPG 847
                                                                                                                                                                                                                                                                                                                                                                                                       EPGEAALHSDSQDGHQMALLNFFFPDEKPYSEEESRRVRRNKRSKSNEGADGPVKNKKKG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177 KKAGPPGPNGPPGPPGP--------PGPGGPPGIPGIP 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   879 PGIGPRGPPGPPGPPGPSFRQDKLTFIDMEGSGFSGDIESLRGPRGFPGPPGVPGVPGLP 938
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  207 GIPGTTVM-----GPPGPPGPPGPPGPPGPPGPPGPPGPSGAADKAGT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92;
                                                                                                                                                                     Query Match 12.7%; Score 267; DB 2; Length 1774; Best Local Similarity 30.2%; Pred. No. 1.2e-09; Matches 71; Conservative 17; Mismatches 55; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 1-19 <RAU>
A;Cross-references: UNIPROT:P02453; UNIPARC:UPI0000173B51
A;Experimental source: skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Residues: 146-294 < FT2>
A; Croses-references: UNIPARC: UP10000173B53
A; Experimental source: skin
R; Fietzek, P.P.; Rexrodt, F.W.; Hopper, K.E.; Kuehn, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Experimental source: skin
R;Wendt, P.; Mark, K.V.D.; Rexrodt, F.; Kuehn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Residues: 295-562 <FI3>
A;Cross-references: UNIPARC:UP10000173B54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: A91387
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A;Title: The covalent structure of collagen. The amino-acid sequence of the 112 residues A;Reference number: A91201; MUID:73042276; PMID:4343808
                                                                                                                                         A; Molecule type: protein
A; Residues: 563-675 < WRN>
A; Residues: 563-675 < WRN>
A; Cross-references: UNIPARC:UP10000173B55
A; Cross-references: WINPARC:UP10000173B55
A; Experimental source: 8kin
B; Fietzek, P.P.; Rexrodt, F.W.; Wendt, P.; Stark, M.; Kuehn, K.
Bur. J. Biochem. 30, 163-168, 1972
A; Fitle: The covalent structure of collagen. Amino acid sequence of peptide alphal-CB6-CA; Reference number: A91200; MUID:73042275; PMID:4343807
A; Accession: A91200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Comment: Lysines at positions 115, 124, 274, 346, 424, 496, 658, and 670 may be hydro: C;Comment: Prolines in the third position of the tripeptide repeating unit (G-X-Y) are i C;Comment: The order of the eight CNBr peptides in the alpha 1(I) chain of bovine skin 9, 149, 268, and 217 residues.
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NiAlternate names: procollagen alpha 1(1) chain
CiSpecies: Homo sapiens (man)
CiSpecies: Homo sapiens (man)
CiSpecies: Homo sapiens (man)
CiDate: 12-Aug-1981 #sequence_revision 04-Oct-1996 #text_change 31-Dec-2004
CiAccession: 160114; S01143; A93335; IS5254; A39943; IS5237; A35233; S09400; B90567; S1 5269; A29439; IS3466; A02852; I37247
SiD'Alessio, M.; Bernard, M.; Pretorius, P.J.; de Wet, W.; Ramirez, F.; Pretorious, P.J.
Gene 67, 105-115, 1988
A;Title: Complete nucleotide sequence of the region encompassing the first twenty-five A;Reference number: 160114; MUID:88329734; PMID:2843432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .comment: The complete chain contains 1052 residues.
Superfemily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homology; Superfemily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal; Keywords: coiled coil; extracellular matrix; glycoprotein; pyroglutamic acid; trimer; 1/Modified site: pyrrolidone carboxylic acid (Gin) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 RSELRRERGAESRLGGSGTPGTSGTLSSLGGLDPDSPITSHLGQPSPKQQPLEPGBAALH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 PAAAPRERGSQG----CGCGGAPARAGE----GNSCLLFLGFFGLSLALHLLTLCCYLEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.7%; Score 266; DB 1; Length 779; 30.0%; Pred. No. 6.1e-10; Live 16; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: protein
A;Residues: 759-779 <RA2>
A;Cross-references: UNIPARC:UP10000173B57
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Biochem. 30, 169-183, 1972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 30.09
Matches 78; Conservative
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R; Baetge, B.; Notbohm, H.; Diebold, J.; Lehmann, H.; Bodo, M.; Deutzmann, R.; Mueller, P. Bur. J. Biochem. 192, 153-159, 1990
A; Title: A critical crosslink region in human-bone-derived collagen type I. Specific cle. A; Reference number: S11372; MUID:90382436; PMID:2169412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Accession: $11372
A,Molecule type: protein
A,Rolecules: 175-187,274-287,'P',289 <BAE>
A,Crose-references: UNIPARC:UPI0000173B40; UNIPARC:UPI0000173B41
A,Note: sequence of collagen alpha 1(S) (I) isolated from bone after pepsin digestion
A,Note: sequence of collagen alpha 1(S) (I) isolated from bone after pepsin digestion
A,Note: sequence of collagen alpha 1(S) (I) isolated from bone after pepsin digestion
A,Bobak, S.B.; Scholz, P.M.; Amenta, P.S.; Constantinou, C.D.; Levi-Minzi, S.A.; Gonzalez
U. Biol. Chem. 266, 21827-21832, 1991
A,Title: The substitution of arginine for glycine 85 of the alpha 1(I) procollagen chain
coperative melting of intact type I collagen.
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A;Nolecule type: mRNA
A;Residues: 258-258;1347-1357 <DBA>
A;Residues: 258-258;1347-1357 <DBA>
A;Cross-references: UNIPARC:UPI0000173B42; UNIPARC:UPI0000173B43; GB:S67495; NID:g239007
A;Cross-references: UNIPARC:UPI0000173B42; UNIPARC:UPI0000173B43; GB:S67495; NID:g239007
A;Note: sequences from the 5' and 3' ends only are shown; mutant sequence 263-Arg report
R;Morgan, P.H.; Jacobs, H.G.; Segrest, J.P.; Cunningham, L.W.
J. Biol. Chem. 245, 5042-5048, 1970
A;Title: Comparative study of glycopeptides derived from selected vertebrate collagens.
A;Reference number: A92069; MUID:71001508; PMID:4319110
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A;Experimental source: Bkin
A;Experimental source: Bkin
A;Experimental Source: Bkin
A;Experiment of 2-O-alpha-D-glucosyl-O-beta-D-galactose to 5-hydroxylysine
B;Labhard, M.E.; Hollister, D.M.
Matrix 10, 124-130, 1990
Mirix 10, 124-130, 1990
Mirix 10, 124-130, 1990
Mirix 10, 124-130, 1990
A;Title: Segmental amplification of the entire helical and telopeptide regions of the cDI
A;Reference number: S15989; MUID:90326017; PMID:2374517
A;Accession: S15989
A;Accession: S15989
A;Accession: S15989
A;Accession: S15989
A;Accession: S15989; MUID:90326017; PMID:26-1045;1143-1162 <LAB>
A;Accession: S15989
A;Accession: S15989
A;Accession: S15989; MID:93339042; PMID:8339541
A;Acference number: I55905; MUID:93339042; PMID:8339541
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A; Molecule type: DNA
A; Residues: 472-594, R., 596-607 < CH3>
A; Residues: 472-594, R., 596-607 < CH3>
A; Cross-references: UNIPARC: UPLO00011F796; GB: K03178; GB: K03179; NID: G179612; NID: G17961
A; Note: the authors translated the codon CGT for residue 595 as Pro
A; Note: the authors translated the codon CGT for residue 595 as Pro
A; Mailis, GAA: Starman, B.J; Zinn, A.B.; Byers, P.H.
Am. J. Hum. Genet. 46, 1034-1040, 1990
A; Title: Variable expression of osteogenesis imperfecta in a nuclear family is explained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: 152205
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Redidues: 342-352, CC, 354-359 «WI2>
A;Cross-references: UNIPARC:UPI0000070EE6; GB:S64717; NID:g408195; PIDN:AAB27677.1; PID:
A;Note: mutant sequence from patient with osteogenesis imperfecta
B;Note: mutant sequence from patient with osteogenesis imperfecta
A;Note: mutant sequence from patient with osteogenesis imperfecta
A;Note: mutant sequence from patient with osteogenesis imperfecta
A;Title: Nucleotide sequences of complementary deoxyribonucleic acids for the proalphal
A;Reference number: A90476; MUID:84080385; PMID:6689127
A;Residues: 162-198,'Z',200-201,'Z',203-206,'Z',208-209,'Z',211-228,'B',230,'BB',233,'Z'
A;Cross-references: UNIPARC:UPI0000173B3F
A;Experimental source: 8kin
A;Note: evidence for 170-allysine
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A,Residues: 425-1250, XX,1252-1328, S',1330-1390, XX,1332-1464 <BER>
A,Residues: 425-1250, XX,1252-1328, S',1330-1390, XX,1332-1464 <BER>
A,Cross-references: UNTPARC:UPT0000017384A; GB:K01228; NID:g180391; PIDN:AAA51995.1; PI
A,Note: sequence partially completed for missing nucleotides by A29439
R;Chu, M.L.; Gargiulo, V.; Williams, C.J.; Ramirez, F.
J, Eld. Chem. 260, 631-634, 1995
A,Title: Multiaxon deletion in an osteogenesis imperfecta variant with increased type
A,Reference number: A22161; MUID:85104934; PMID:2981843
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Residues: 263-268 <MOR>
Cross-references: UNIPARC:UP1000014DF11
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A;Residues: 1-45 <ROS.
A;Coss-references: UNIPARC:UPIO00016A6B2; GB:J02829; NID:g180387; PIDN:AAA51993.1; PID: A;Residues: 1-45 <ROS.
A;Cross-references: UNIPARC:UPIO00016A6B2; GB:J02829; NID:g180387; PIDN:AAA51993.1; PID: R;Bornstein, P:; McKay, J:; Morishima, J.K.; Devarayalu, S.; Gelinas, R.E.
Proc. Natl. Acad. Sci. U.S.A. 84, 8869-8873, 1987
A;Title: Regulatory elements in the first intron contribute to transcriptional control of A;Reference number: A39943; MUID:88097389; PMID:3480516
A;Accession: A39943
A;Accession: A39943
A;Residues: 1-34 <BOR.>
A;Residues: 1-34 <BOR.>
A;Reference number: MuiD:881097389; PMID:2857713
A;Cross-references: UNIPARC:UPIO00016A6B1; GB:J03559; NID:g180876; PIDN:AAA52052.1; PID: A;Title: Pine structural analysis of the human pro-alpha 1 (I) collagen gene. Promoter 8
A;Accession: 155237; MUID:85130970; PMID:2857713
A;Accession: 155237
A;Residues: 1-34 <CH2.>
A;Accession: 155237
A;Ac
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A; Accession: A35233
A; Accession: A35233
A; Accession: A35233
A; Mulbecule type: protein
A; Residues: 33-52
A; Cross-references: UNIPARC: UPI0000173B3D
A; Cross-references: UNIPARC: UPI0000173B3D
A; Cross-references: UNIPARC: UPI0000173B3D
A; Tile: A base substitution in the exon of a collagen gene causes alternative splicing
A; Reference number: 809400
A; Accession: 809400
A; Molecule type: mRNA
A; Residues: 156-183
A; References: UNIPARC: UPI0000173B3E
B; Click, E.M.; Bornstein, P.
A; Residensistry 9; 4699-4706; 1970
A; Reference number: A90567; MUID:71038625; PMID:5529814
A; Cross-tents: CNBEO-1, CNBEC, CNBEC, CNBEC, A; A; CORDE-1, CNBEC, CNBEC
                     A,Accession: 160114
A,Scrutte: translated from GB/EMBL/DDBJ
A,Scrutte: translated from GB/EMBL/DDBJ
A,Scrutte: translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-369, 'L',371-589 < DAL>
A,Kocession: UNIPROT:0202453; UNIPROT:0216053; UNIPROT:021896; UNID:021828; UNIPROT:021896; UNID:021828; UNIPROT:021896; UNID:021828; UNID:02182
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C;Accession: $16366
R;Pettitt, J.; Kingston, I.B.
3, Title: The complete primary structure of a nematode alpha-2(IV) collagen and the partit A;Reference number: $16366; MUD:91340768; PMID:1714907
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A;Cross-references: UNIPROT:P53420; UNIPARC:UPI000000769; GB:X81053; NID:g574805; PIDN:
R;Sugimoto, M.; Oohashi, T.; Yoshioka, H.; Matsuo, N.; Ninomiya, Y.
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P;43-1529/Domain: collagenous #status predicted <COL>
P;197-199/Region: cell attachment (R-G-D) motif
P;1530-1763/Domain: carboxyl-terminal nonhelical, NCI #status predicted <NCIL>
P;1530-1763/Domain: repeat NCI #status predicted <NCIL>
P;1539-1763/Domain: repeat NCI #status predicted <NCIL>
P;133-134,39,41,536,539/Disulfide bonds: interchain #status predicted
P;126/Binding site: carbohydrate (Asn) (covalent) #status predicted
P;1593-1599,1702-1709/Disulfide bonds: #status predicted
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                                                                                                                                  collagen alpha 2(IV) chain precursor - pig roundworm
C;Species: Ascaris suum (pig roundworm)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
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F:27-1763/Product: collagen alpha 2(IV) chain #status predicted <MAT>
F:27-42/Domain: non-collagenous NH1 #status predicted <NH1>
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                                                                                                                             - pig roundworm
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446 AKGEPGPR 453
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A; Reference number: A35356, MUID:9025792; PMID:2339700
A; Accession: A35336
A; MOLECULE Urpe: mRN
A; Reference number: A35336
A; MOLECULE Urpe: mRN
A; Roce: the authors translated the codons GAG for 721 and CGT for 738 as Glu
A; NOCE: the authors translated the codons GAG for 721 and CGT for 738 as Glu
B; NOCE: the authors translated the codons GAG for 721 and CGT for 738 as Glu
R; Portino, A; Zolezzi, F; Valli, M; Pignatti, P. P; Cetta, G; Brunalli, P. C.; Mottes
Hum, Wol. Genet. 7, 2201-2206, 1394
A; Titla: Severe (type III) Osteogenesis imperfects due to glycine substitutions in the A; Reference number: 154365; MUID:95187161; PMID:7881420
A; Titla: Severe (type III) Osteogenesis imperfects due to glycine substitutions in the A; Reference number: 154365; MUID:95187161; PMID:994897
A; Cross-references: UNIPARC:UPPONOUT666A; GB:L47667; NID:gl00903; PIDN:ABS9576.1; PID
A; A; Reference number: A4726; MUID:9335646; PMID:994897
A; Reference contracted from RGB! backbone (NCDIN:11644, NCSIR:116445)
A; Roce: Generic contracted from RGB! backbone (NCDIN:11644, NCSIR:116445)
A; Roce: Generic contracted from RGB! backbone (NCDIN:11644, NCSIR:116446, NCSIR:118446, NCSIR:118446
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Qy 175KCKKAGPPGPNGPGP : : Db 1215 PGSPGISPPGPRGKGPPGPPGSSGPPGPAGA	Qy 203 PGIPGIPGTTVMGPPGPPGPPQPDQU : :	Search completed: January 13, 2006, 16:15:22 Job time : 17 secs										
FEBS Lett. 330, 122-128, 1993 A;Title: cDNA isolation and partial gene structure of the human alpha-4(IV) collagen cha A;Reference number: S36854; MUID:93374047; PMID:8365481	A;Molecule type: DNA; mRNA A;Molecule type: DNA; mRNA A;Residues: 1219-1658, FE', 1661-1690 <sug> A;Cross-references: UNIPARC:UPID000016A432; DDBJ:D17391; NID:g440365; PIDN:BAA04214.1; PI</sug>	Ajaxperimental Bource: Winone ye Kramagata, Y.; Mattei, M.G.; Minomiya, Y.; Kamagata, Y.; Mattei, M.G.; Minomiya, Y. J. Biol. Chem. 267, 23753-23758, 1992 A;Title: Isolation and sequencing of CDNAs and genomic DNAs encoding the alpha4 chain of A;Reference numbers: \$28777; MUID:93054733; PMID:1429714	A; Molecule type: DNA A; Residues: 1407-1424, 'G', 1426-1430, 'A', 1432-1439, 'L', 1441-1507 <kam>A; Residues: 1407-1424, 'G', 1426-1430, 'A', 1432-1475; GB:LO1476 A; Cross-references: UNIPARC: UPI0000173BFC; GB:LO1475; GB:LO1476 A; Note: the codons given for 1438-Asp (GAG) and 1443-Gly (GCA) are inconsistent with the C; Comment: Prolines and lysines at the third position of the tripeptide repeating unit (C; Genetics:</kam>	A;Gene: GDB:CO14A4 A;Gross-references: GDB:132673; OMIM:120131 A;Map position: 2q35-2q37 A;Introns: 39/1; 1406/1; 1445/1; 1508/1; 1603/3 #status incomplete A;Note: the alpha 3(1V) and alpha 4(1V) chain genes are encoded on opposite strands with C;Complex: this minor type IV collagen is thought to form a heterotrimer of two alpha 3(mong trimer amino-terminal domains (with disulfide and desmosine cross-links), dimeric a er associations in the interrupted helical domain (with disulfide and desmosine cross-li	C;Function: minor structural component of extracellular basement membrane in kidney g A;Description: minor structural component of extracellular basement membrane in kidney g C;Superfamily: collagen alpha 1(IV) chain C;Superfamily: collagen alpha 1(IV) chain C;Reywords: basement membrane; coiled coil; extracellular matrix; glycoprotein; hydroxyl F;139-1690/Panain: salpal sequence #status predicted cSIG> F;39-1690/Product: collagen alpha 4(IV) chain #status predicted cMAT> F;39-16/Domain: amino-terminal nonhelical, NH1 cNH1>	Fig2-1466/Region: interrupted felical Fig24-56/Region: cell attachment (R-G-D) motif Fil89-191/Region: cell attachment (R-G-D) motif Fil89-191/Region: cell attachment (R-G-D) motif Fil89-191/Region: cell attachment (R-G-D) motif Fil80-1312/Region: cell attachment (R-G-D) motif Fil80-187/Region: cell attachment (R-G-D) motif Fil80-191/Region: cell attachment (R-G-D) motif Fil80-191/Region: cell attachment (R-G-D) motif Fil80-1690/Domain: carboxyl-terminal nonhelical, NC1 <nc1> Fil87-1690/Domain: collagen IV carboxyl-terminal repeat <ct1> Fil879-1686/Domain: collagen IV carboxyl-terminal repeat <ct2></ct2></ct1></nc1>	F;47,52,55,57,266,400,460,492,494,668,790,828,1095,1]31,1294,1317,1375,1407/Disulfide bd F;142,669/Bhinding afte: carbohydrate (Apan) (covalent) #status predicted F;1480-1566,1513-1569/Disulfide bonds: (or 1480-1569, 1513-1569/Disulfide bonds: (or 1480-1569, 1513-1569/Bisulfide bonds: #status predicted F;1525-1531,1634-1641/Disulfide bonds: #status predicted F;1588-1683,1622-1686/Disulfide bonds: (or 1588-1686, 1622-1683) #status predicted	Query Match 12.6%; Score 264; DB 1; Length 1690; Best Local Similarity 27.4%; Pred. No. 1.8e-09; Matches 96; Conservative 18; Mismatches 96; Indels 140; Gaps 15;	Oy 2 GYPEVERRELLPAAAPRERGSQG-CGCGGAARAGEGNSCLLFLGFFGLSLALHLLTLCC 60	Qy 61 YLELRSELRRERGAESRLGGSGTPGTSGTLSSLGGLDPDSPITSHLGGPSPKQQPLEPG- 119	Qy 120 EAALHSDSQDGHQWALLNPFPPDEK 144 Db 1096 PGHPGASGEQGLPGIQGPRGSPGRPGPSSGPPGCPGDHGMPGLR-GQPGEMGDPGPRG 1154	Qy 145KNKK 174 Db 1155 LQCDPGIPGPPGIKGPSGSPGLNGLHGLKGQKGTKGASGLHDVGPPGPVGIPGLKGERGD 1214

175KGKKA-GPPGPPGPPGPPGPPGPPGI 202	1215 PGSPGISPPGPRGKKGPPGPPGSSGPPGPAGATGRAPKDIPDPGPPGDQGPPGPPGPRGA 1274	203 PGIPGIPGTTVMGPPGPPGPPGPPGPGGPPGLAGPR 244	1275 PGPPGLPGSVDLLRGEPGDCGLPGPPGPPGPPGPPGYKGPPGCDGKDGQK 1324	
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ALIGNMENTS

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TISSUE=Sweat gland;
MEDLINE=96331280; PubMed=8696334;
MEDLINE=96331280; PubMed=8696334;
Kere J., Srivastava A.K., Montonen O., Zonana J., Thomas N.S.T.,
Ferguson B.M., Munoz F., Morgan D., Clarke A., Baybayan P., Chen B.Y.,
Ezer S., Saarialho-Kere U., la Chapelle A., Schlessinger D.;
"X-linked anhidrotic (hypohidrotic) ectodermal dysplasia is caused by
mutation in a novel transmembrane protein.";
Nat. Genet. 13:409-416(1996).
                                                                                                                                                                                                                                                                                                                                 [1] -
NUCLEOTIDE SEQUENCE [GENOMIC DNA / MRNA] (ISOFORM I), AND VARIANTS EDA
HIS-61 AND LEU-69.
                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [4]

WUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

PUBMEd=15772651; DOI=10.1038/nature03340;

ROSS M.T., Grafham D.V., Coffey A.J., Scherer S., McLay K., Muzny D.,

Platzer M., Howell G.R., Burrows C., Bird C.P., Frankish A.,

Lovell F.L., Howe K.L., Ashurst J.L., Fulton R.S., Sudbrak R., Wen G.,

Jones M.C., Hurles M.B., Andrews T.D., Scott C.E., Searle S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-98409495; PubWed-9736768; DOI=10.1093/hmg/7.11.1661; Bayes M., Hartung A.J., Ezer S., Pispa J., Thesleff I., Srivastava A.K., Kere J.; Pispa J., Thesleff I., The anhidrotic ectodermal dysplasia gene (EDA) undergoes alternative splicing and encodes ectodysplasin-A with deletion mutations in collagenous repeats.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [3]
NUCLEOTIDE SEQUENCE (ISOFORMS A1; A2; B; C; D; E AND F), AND VARIANTS
                                                                             01-NOV-1997 (Rel. 35, Created)
15-UL-1999 (Rel. 38, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Ectodysplasin A (Ectodermal dysplasia protein) (EDA protein)
[Contains: Ectodysplasin A, membrane form; Ectodysplasin A, secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MISSURELiver;
MEDLINE-98349961; PubMed-9683615;
Monreal A.W., Zonana J., Ferguson B.M.;
Monreal A.W., Zonana J., Ferguson B.M.;
Identification of a new splice form of the EDA1 gene permits
detection of nearly all X-linked hypohidrotic ectodermal dysplasia
mutations.";
                     EDA HUMAN STANDARD; PRT; 391 AA.
Q92838; 075910; Q5JUM7; Q9UP77; Q9X6L0; Q9X6L1; Q9Y6L3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [2]
NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM A1), AND VARIANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hum. Mol. Genet. 7:1661-1669 (1998).
                                                                                                                                                                                                       Name=EDA; Synonyms=ED1;
                                                                                                                                                                                                                                                                                         Homo.
NCBI_TaxID=9606;
                                                                Q9Y6L4;
                                                                                                                                                                                        form)
EDA HUMAN
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Mol. Genet. 10:953-962(2001).

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RECEPTOR INTERACTION (ISOPORMS A1 AND A2).

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                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 230-391, AND SUBUNIT
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Comment=Additional isoforms seem to exist;
                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 98:7218-7223(2001)
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MEDLINE=98292028; Pubmed=9630076;
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                                                                                                                          AALHSDSODGHOMALLNFFFPDEKPYSEEESRRVRRNKRSKSNEGADGPVKNKKKGKKAG
                                                                                                                                   AALHSDSQDGHQMALLNFFFPDEKPYSEESRRVRRNKRSKSNEGADGPVKNKKKGKKAG
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Q9BEG5; Q9BEG6;

28-FEB-2003 (Rel. 41, Created)

28-FEB-2003 (Rel. 41, Last sequence update)

13-SEP-2005 (Rel. 48, Last annocation update)

Estedoysplasin A (Estedoysplasin 1) (Estedosmal dysplasia protein)

[Çonțains: Estedoysplasin A, membrane form; Estedoysplasin A, secreted
                                         Gapa
                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
Eukāryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
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                        Length 391;
                                        Indels
Name=1;
IsoId=Q92838-2; Sequence=VSP_006454, VSP_006455;
                      Score 2098; DB 1;
Pred. No. 3.6e-115;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
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NUCLEOTIDE SEQUENCE (ISOFORMS A1 AND A2).
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                       100.0%;
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                                        Matches 391; Conservative
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                                Similarity
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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PTM: N-glycosylated (By similarity).

PTM: Processing by furin produces a secreted form (By similarity).

DISEASE: Defects in EDA are the cause of anhidrotic ectodermal adysplasia. The disease is characterized by sparse hair (atritchosis or hypotrichosis), abnormal or missing teeth and the inability to sweat due to the absence of sweat glands.

SIMILARITY: Belongs to the tumor necrosis factor family.

SIMILARITY: Contains 1 collagen-like domain.
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Cytoplasmic (Potential).
Cytoplasmic (Potential).
Signal-anchor for type II membrane
protein (Potential).
Extracellular (Potential).
Collagen-like.
Cleavage (by furin) (By similarity).
N-linked (GlcNAc. . ) (Potential).
N-linked (GlcNAc. . ) (Potential).
Missing (in isoform A2).
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form (By
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PROSITE; PS0049; TNF 2; 1.
Alternative splicing; Collagen; Developmental protein;
CHEFrentiation; Glycoprotein; Ectodysplasin A, membrane.
CHAIN 160 391 Ectodysplasin A, secreted form.
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Pred. No. 8.6e-108;
4; Mismatches 18;
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EMBL, AJ300469; CAC29151.1; OJUNED; Genomic_DNA.
EMBL, AJ300469; CAC29151.1; JOINED; Genomic_DNA.
EMBL, AJ300468; CAC29152.1; -; Genomic_DNA.
EMBL, AJ300469; CAC29152.1; -; Genomic_DNA.
EMBL, AJ300469; CAC29152.1; JOINED; Genomic_DNA.
EMBL, AJ300409; CAC29152.1; JOINED; Genomic_DNA.
SWR; Q9BEG5; 242-390.
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InterPro; IPROO6652; TNP family.
Pfam; PPO1391; Collagen; 1.
Pfam; PF00229; TNF; 1.
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Mech. Dev. 88:133-146(1999).
-!- FUNCTION: Involved in epithelial-mesenchymal signaling during morphogenesis of ectodermal organs. Isoform TAA binds only to the receptor EDAR, while isoform TA-A2 binds exclusively to the receptor XEDAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTM: N-glycosylated (By similarity).

PTM: N-glycosylated (By similarity).

PTM: Processing by furin produces a secreted form (By similarity)
                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Embryo;
MEDINE=20005791; PubMed=10534613; DOI=10.1016/S0925-4773(99)00180-X;
MIKKOIM M.L., Pispa J., Pekkanen M., Paulin L., Nieminen P., Kere J.,
Thealeff I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene: evidence
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WUCLEOTIDE SEQUENCE (ISOFORM TAD).
MEDLINE=97449184; PubMed=9285798; DOI=10.1093/hmg/6.9.1589;
Perguson B.M., Brockdorff N., Formstone E., Ngyuen T.,
Kronmiller J.E., Zonana J.;
Kronmiller J.E., Zonana J.;
"Cloning of Tabby, the murine homolog of the human EDA gene: evidence for a membrane-associated protein with a short collagenous domain.";
Hum. Mol. Genet. 6:1589-1594(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (B)
                                                                                                                                                                                                                                                                                                                        STRAIN=129/Sv;
MEDLINE=98068770; PubMed=9371801; DOI=10.1073/pnas.94.24.13069;
Srivastava A.K., Pispa J., Hartung A.J., Du Y., Ezer S., Jenks T.,
Srivastava A.K., Pispa J., Hartung A.J., Du Y., Ezer S., Jenks T.,
Shimada T., Pekkanen M., Mikkola M.L., Ko M.S.H., Thesleff I.,
Kere J., Schlessinger D.;
"The Tabby phenotype is caused by mutation in a mouse homologue of "The Tabby phenotype is caused by mutation in a mouse homologue of protein (ectodysplasin-A) with collagenous domains.";
Proc. Natl. Acad. Sci. U.S.A. 94:13069-13074(1997).
                                                                                                         EDA MOUSE STANDARD; PRT; 391 AA.

O54693; O35705; Q9QWJ8; Q9QZ01; Q9QZ02;
15-JUL-1999 (Rel. 38, Created)
13-SEP-2005 (Rel. 48, Last acquence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Ectodysplasin A (EDA protein homolog) (Tabby protein) [Contains: Ectodysplasin A, membrane form; Ectodysplasin A, secreted form].

Name=Eda; Synonyms=Ed1, Ta;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- SUBUNIT: Homotrimer (By similarity).
-i- SUBCELLUIAR LOCATION: Type II membrane protein and secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=054693-3; Sequence=VSP_006469, VSP_006471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isold=054693-4; Sequence=VSP_006466, VSP_006467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isold=054693-5; Sequence=VSP_006465, VSP_006468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=6;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE (ISOFORMS TAA; TAB AND TAC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE (ISOFORMS TA-A2 AND TA-A3).
                  361 AVXMVHADISINMSKHTTFFGAIRLGEAPAS 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=054693-6; Sequence=VSP_006470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=054693-2; Sequence=VSP_006471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=TAA; Synonyms=A1;
IsoId=O54693-1; Sequence=Displayed;
                                   361 AVKMVHADISINMSKHTTFFGAIRLGEAPAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity).
ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=TA-A2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=TA-A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=TAB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=TAC;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VACACLETION TAC), FTIG=VSP_006465.

FTIG=VSP_006465.

FTIG=VSP_006466.

Missing (In isoform TAB).

FTIG=VSP_006467.

Missing (In isoform TAC).

Missing (In isoform TAC).

FTIG=VSP_006466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-linked (GlcNAc. .) (Potential).
MALLNPFFPDERAYSEBESRRVRNKRSKSBGADGPVKNK
KKGKKAGPPGPPGPPGPPGPPGPPGPPGTTTVM
GPPGPPGPGPGLGGPSGAA -> VSHLGGAAALEAP
SPARLGGGLRAGGTLPLRAKFQGRSWEWAGVLGRGCPGQ
VVLGSCLGSSRPSPVPWSWKAQPARAAPGEVWAA (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Missing (In isoform TA-A2 and isoform TA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R Bnsembl; ENSWIGSGO000059327; Mus musculus.

R MGI: MGI:1195272; Eda.

R GO; GO:0045177; C:apical part of cell; IDA.

R GO; GO:006589; C:andoplasmic reticulum membrane; IDA.

R GO; GO:0007160; P:cell-matrix adhesion; IDA.

R GO; GO:0007160; P:cell-matrix adhesion; IDA.

R GO; GO:000731; P:salivary gland development; IDA.

R HO; GO:0007431; P:salivary gland development; IDA.

R InterPro; IPR008160; Collagen.

R InterPro; IPR006052; TNF_family.

R PF00729; TNF: 1.
-!- DISEASE: Defects in Eda are the cause of the tabby phenotype in mice (the equivalent of anhidrotic ectodermal dysplasia in humans). The disease is characterized by sparse hair (atrichosis or hypotrichosis), abnormal or missing teeth and the inability to sweat due to the absence of sweat glands.
-!- SIMILARITY: Belongs to the tumor necrosis factor family.
-!- SIMILARITY: Contains 1 collagen-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytoplasmic (Potential).
Signal-anchor for type II membrane signal-anchor for type II membrane protein (Potential).
Extracellular (Potential).
Collagen-like.
Cleavage (by furin) (By similarity).
N-linked (GlcNAc. .) (Potential).
N-linked (GlcNAc. .) (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00251; TNF_1; FALSE_NEG.
PROSITE; PS50049; TNF_2; 1.
Alternative splicing; Collagen; Developmental protein;
Differentiation; Glycoprotein; Signal-anchor; Transmembrane.
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ectodysplasin A, membrane form. Ectodysplasin A, secreted form similarity).
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EMBL, AF016629, AAB95203.1; -; MRNA.
EMBL, AF016629, AAB95203.1; -; MRNA.
EMBL, AF016630, AAB95205.1; -; MRNA.
EMBL, AF016631, AAB95205.1; -; MRNA.
EMBL, AF016434, AAB95205.1; -; MRNA.
EMBL, AF004434, AAB98121.1; -; Genomic_DNA.
EMBL, X13439, CAA73849.1; -; MRNA.
EMBL, AJ243657, CAB52696.1; -; MRNA.
EMBL, AJ243659; CAB52696.1; -; MRNA.
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/FTId=VSP
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Pfam; PF00229; TNF; 1.
PROSITE; PS50049; TNF_2; 1.
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NUCLEOTIDE SEQUENCE.
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Thutation identification in a canine model of X-linked ectodermal
dysplasia.";

Gyaplasia.";

Gyaplasia.";

Rubi. AX924414; AAX38257.1; Genomic. DNA.

EMBL; AX924407; AAX38257.1; JOINED; Genomic. DNA.

REMBL; AX924410; AAX38257.1; JOINED; Genomic. DNA.

REMBL; AX924410; AAX38257.1; JOINED; Genomic. DNA.

REMBL; AX924410; AAX38257.1; JOINED; Genomic. DNA.

REMBL; AX924413; AAX38257.1; JOINED; Genomic. DNA.

REMBL; AX924411; AAX38257.1; JOINED; Genomic. DNA.
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                                                                                                                           Gaps
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10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
Name=BDA;
Cania familiaris (Dog).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
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GG; GG:0016020; C:membrane; IEA.
GG; GG:0016020; C:membrane; IEA.
GG; GG:0006955; P:tumer necrosponse; IEA.
GG; GG:0006955; P:tumune response; IEA.
GG; GG:0006817; P:phosphate transport; IEA.
InterPro; IPR0008160; Collagen.
InterPro; IPR0008162; TNF family.
PF01191; Collagen; 1.
                                                                              Length 391;
                                                                                                                           Indels
         126 D -> E (in Ref. 2).
41603 MW; E5ECEDASBD60DBFP CRC64;
                                                                       Query Match
93.7%; Score 1965; DB 1;
Best Local Similarity 94.6%; Pred. No. 2.2e-107;
Matches 370; Conservative 1; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 AVKMVHADISINMSKHTTFFGAIRLGEAPAS 391
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QS8P77;
            126 1
391 AA;
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NUCLEOTIDE SEQUENCE.
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         CONFLICT
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                                                                                                                                                                                                                                            YLELRSELRRERGAESRIGGSGTPGTSGTLSSLGGLDPDSPITSHLGQPSPKQQPLEPGE 120
                                                                                                                                                                                                                                                                        61 YLELRSELRRERGAESRLG----PGTPGTLNSPGGLDPDGPITRDSGQPSPQQQPLBAEE 116
                                                                                                                                                                                                                                                                                                                                     121 AALHSDSQDGHQMALLNFFFPDEKPYSEBESRRVRRNKRSKSNEGADGPVKNKKKGKKAG 180
                                                                                                                                                                                                                                                                                                                                                                       181 PPGPNGPPGPPGPPGPPGIPGIPGIPGTTVMGPPGPPGPPGPPGPPGLQGPSGAADK 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Houghton L., Morgan B.A.;

Rubmitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.

Bubmitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.

RMSI, AV885699; AAW81692.1; -; mRNA.

SWR; GSEZS; 207-335.

R GO; GO:0005737; C:cytroplasm; IEA.

R GO; GO:0005737; C:cytroplasm; IEA.

R GO; GO:0005164; F:tumure response; IEA.

R GO; GO:0006955; P:tmmune response; IEA.

R GO; GO:0006955; P:tmmune response; IEA.

R InterPro; IPR008160; COllagen.

R InterPro; IPR008160; COllagen.

R Pfam; PF01391; COllagen; I.

R Pfam; PF01391; COllagen; I.

R Pfam; PF00229; TNF; L.
                                                                                              .;
2
                                             90.1%; Score 1890.5; DB 2; Length 386; 91.3%; Pred. No. 5e-103; ive 8; Mismatches 21; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         356 AA; 37526 MW; 8D53PD97F71FDDFB CRC64;
386 AA; 41235 MW; 6095BDBC3EACP68B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 AVKWVHADISINMSKHTTFFGAIRLGEAPAS 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    356 AVKWYHADISINMSKHTTFFGAIRLGEAPAS 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      356 AA
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10-MAY-2005 (TrEMBLrel. 30, L
10-MAY-2005 (TrEMBLrel. 30, L
Ectodysplasin Al (Fragment).
Name=Eda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OSEFZS_CHICK PRELIMINARY;
                                                Query Match
Best Local Similarity 91.34
Matches 357; Conservative
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YLELRSELRRERGAESRLGGSGTPGTSGTLSSLGGLDPDSPITSHLGQPSPKQQPLEPGE 120
                                                                                                                                       PQGPPGIPGIPGIPGTTVMGPPGPPGPPGPQGPPGLQGPSGAADKAGTRENQPAVVHLQG 255
                                                                                                                                                                              QGSAIQVKNDLSGGVLNDWSRITMNPKVFKLHPRSGELEVLVDGTYFIYSQVEVYYINFT 315
                                                                                                                                                                                                                                    DFASYEVVVDEKPFLOCTRSIETGKTNYNTCYTAGVCLLKARQKIAVRAVHADISINMSK 375
        GTSGTLSSLGGLDPDSPITSHL-GQPSPKQQPLEPGEAALHSDSQDGHQMALLNFFFPDE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         roumo aproces, Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Merazoa; Chordata; Craniata; Primates; Catarrhini; Hominidae;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 178;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clark S.; Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases. Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases. EMBL; AL450449; CA139805.1; -; Genomic_DNA. EMBL; AL158069; CA139805.1; JOINED; Genomic_DNA. EMBL; AL450449; CA139805.1; JOINED; Genomic_DNA. EMBL; AL450449; CA131611.1; JOINED; Genomic_DNA. EMBL; AL450449; CA141611.1; JOINED; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Whitehead S.; Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                         10-MAY-2005 (TrEMBLrel. 30, Created)
10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 887; DB 2; L
Pred. No. 1.4e-44;
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                                                                                                                                                                                                                                                                                                                                                                                                178
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Name=EDA; ORFNames=RP11-351K23.1-003;
Homo sapiens (Human).
                                                                   KPYSEEESRRVRRNKRSKSNEGADGPV-
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HTTFLGSVRLGEAPSA 364
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QSJSOO;
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                                                                                                                                                                                                                                                                                                                             QVEVYYINFIDFASYEVVVDEKPFLQCTRSIETGKTNYNTCYTAGVCLLKARQKIAVKMV 365
                                                                                                                                                      128 QDGHQMALLINFFFPDEKPYSEEESRRVRRNKRSKSNEGADGP--VKNKKKGKKAGPPGPN 185
                                                                                                 RRERGAESRLGGSGTPGTSGTLSSLGGLDPDSPITSHLGQPSPK-QOPLEPGRAALHSDS 127
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                                                                                                                                                                                                                                                                      246 NOPAVVHLQGQGSAIQVKNDLSGGVLNDWSRITMNPKVFKLHPRSGELEVLVDGTYFIYS
                                                                                                                                                                                                                                                                                     211 TQPAVVHLQGQGSAIQVKNDLSGGVLNDWSRITMNPKVFKLHARSGELEVLVDGTYFIYS
                                                                                                                                                                                                                                                                                                                                            25 CGCGGAPARAGEGNSCLLFLGFFGLSLALHLLTLCCYLELRSELRRERGAESRLGGSGTP
                                                        54 RRDRGPQP----AAPPRRDGTAAAA---PGAP-----PAVRPQRPAESGERR----
                                         13 PAAAPRERGSQ----GCGCGGAPARAGEGNSCLLFLGFFGLSLALHLLTLCCYLELRSEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "widespread parallel evolution in sticklebacks by repeated fixation Ectodysplasin alleles.";
Science 307:1928-1933(2005).
Science 307:1928-1933(2005).;
InterPro; IPR009160; Collagen.
InterPro; IPR006052; TNF family.
Pfam; PF01991; Collagen; 1.
              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gasterosteus aculeatus (Three-spined stickleback).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostcmi;
Actinopteryydi; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteides;
Gasterosteidae; Gasterosteus.
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              37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=15790847; DOI=10.1126/science.1107239;
Colosimo P.F., Hosemann K.E., Balabhadra S., Villarreal G. Jr,
Dickson M., Grimwood J., Schmutz J., Myers R.M., Schluter D.,
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              41; Indels
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 45.5%; Score 955.5; DB 2; Best Local Similarity 51.1%; Pred. No. 2.8e-48; Matches 192; Conservative 59; Mismatches 86;
 Pred. No. 9.2e-77;
; Mismatches 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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.larity 74.9%; Pr
Conservative 19;
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OSODS4;
13-SEP-2005 (TEMBLrel. 31,
13-SEP-2005 (TEMBLrel. 31,
13-SEP-2005 (TEMBLrel. 31,
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  Similarity
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Name=Eda;
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SEQUENCE
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 Best Local 9
Matches 289
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Q8VIF6_MOUSE PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., May J.M., Brunet F., Detit J.L., Stange-Thomann N., Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Micaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Sequrens B., Daslava C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V., Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J., Kellis M., Volff JN., Guigo R., Zody M.C., Mesirov J., McEwan P., Bosak S., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Lindblad-Toh K., Sharren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Wincker P., Lander E.S., Weissenbach J., Roest Crollius H., "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 GPPGPPGPPGPPGPPGIPGIPGTTVMGPPGPPGPPGPPGPPGLQGPSGAADKAGTRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GPPGPPGPPGPQGPPGIPGIPGIPGSNVVGPVGPPGPPGPQGPPGTQGPAGDPDKTKTRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                          OKTNAMES-GSTENGO0017090001;
Tetraodon nigroviridis (Green puffer).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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Genoscope; Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.

-I- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which preliminary data.

EMBL, CAADO1014573. CAP99121.1; -; Genomic_DNA.

InterPro; IPR006160; Collagen.

InterPro; IPR006652; TNF family.

Pfam; PF01391; Collagen: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 38.6%; Score 809; DB 2; Length 20 Best Local Similarity 68.9%; Pred. No. 6e-40; Matches 142; Conservative 32; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22149 MW; 6CB874AF177DA5CA CRC64;
                                                                                                                 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome 1 SCAF14573, whole genome shotgun sequence.
               207 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the early vertebrate proto-karyotype.";
Nature 431:946-957(2004).
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                                                                                   (TrEMBLrel. 31, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00251; TNF_1; UNKNOWN_1.
PROSITE; PS50049; TNF_2; 1.
           Q4SJR1_TETNG PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207
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207 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=99883;
                                                                                   13-SEP-2005
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SEQUENCE
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               SOTIAN SOCIAL SECTION SOCIAL SECTION
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494 GE------RGSKGSKGSKGSRGSPGKPGPQGPSGDPGPPGKDGLPG 539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196 PQGPPGIPGI-----PGIPGTT-VMGPPGPPGPGPQGPPGLQGPSGAADKAGTRENQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                540 PQGPPGPGQGTVGEPGVPGPRGLPGLPGVPGMPGPKGPPGPPGPSGAMEPLAL-QNEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 GTPGTSGTLSSLGGLDPDSPITSHLGQPSPKQQPLEPGEAALHSDSQDGHQMALLNPPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    443 GPPGPRGPRGDRGSQGPPGP-TGNKGQKGEKGEPGPPGPA-----GERGTIGPVGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 DEKPYSEBESRRVRRNKRSKSNEGADGPVKNKKKGKKAGPPGPNGPPGPPGP-----PG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     599 T------BASEV-----NGCPPHWKNFTDKCYYFSL-----EKELLEDAKLFC----
                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.6%; Score 286; DB 2; Length 742; 30.5%; Pred. No. 9.2e-09; Live 29; Mismatches 96; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    742 AA; 81306 MW; 85A90D3AE881DB6B CRC64;
                                            Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        309 VYYINFIDFASYEVVVDEKPFLOCTRSIETGKTNY 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----BDKSSHLVFINSREEQQWIKKHTVGRESH 664
                               01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last seque
01-MAR-2004 (TrEMBLrel. 26, Last annol
Scavenger receptor with C-type lectin
PRT;
                                                                                                Name=Colec12; Synonyms=srcl;
Mus musculus (Mouse).
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                                                                                                                                                                           NCBI_TaxID=10090;
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RESULT 9 Q8VIF6_MOUSE

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TISSUE-MARMERY TUNDER.

TISSUE-MARMERY TUNDER.

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TISSUE-MARMERY TUNDER.

THEOLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Strausberg R.L., Feringold E.A., Grouee L.H., Derge J.G.,

Riausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

A Distchenco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glabs R.A.,

A Halton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Raha S.C., Grimwood J., Schmutz J., Myers R.M.,

B Bakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

B Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

B Cheneration and linital analysis of more than 15,000 full-length human

T "Generation and linital analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 DGHQMALLINFFFPDEKPYSEEESRRVRRNKRSKSNEGADGPVKNKKKGKKAGPPGPNGPP 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 RRERGAESRLGGSGTPGTSGTLSSLGGLDPDSPITSHLGQPSPKQQPLEPGEAALHSDSQ 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----GGRGLPGPPGN----NGNPGPPGPSGAP 654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                579 KGERGAPGEKGEGGPPGPAGPTGSSGPAGPPGP----QGVKGERGSPGGPGTAG-----
                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
REMBL; BC013656; AAH13626.1; -; mRNA.
REMBL; BC013656; AAH13626.013a1.
RGJ; MGI: MGI: MGI; C:cytoplasm; IEA.
GG; GO:0006817; P:phosphate transport; IEA.
R InterPro; IPR008160; Callagen.
R InterPro; IPR008160; Callagen.
R Pfam; PF01391; Collagen, 12.
R Propom; PD000007; C1g_helix; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Mix FVB/N;
TISSUE=Mammary tumor. WAP-TGF alpha model. 7 months old;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      998 AA; 95451 MW; 2AB4BA953B7084A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        548 PRGGPGERGEHGPPGPAGFPGAPGQNGEPGA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                       01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
               998 AA.
               PRT;
                                           Created)
                                        01-MAR-2003 (TrEMBLrel. 23,
                                                                                    Col3al protein (Fragment).
Name=Col3al;
         QBCFM4_MOUSE PRELIMINARY;
QBCFM4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
tes 87; Conserv
                                                                                                                                                                                                                   STRAIN=Mix FVB/N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Collagen.
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Matches
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Universe to the EMBL/GenBank/DDBJ databases.

Submitted (SEP-2003) : .; mRNA.

EMBL; AB078434; BAC05523.1; -; mRNA.

EMBL; BC057936; AAH57936.1; -; mRNA.

EMBL; BC057936; AAH57936.1; -; mRNA.

EMBL; BC057936; AAH57936.1; -; mRNA.

EMBL; BC057936; Colec12.

Ensembl; ENSWUSGO000036103; Mus musculus.

MG1; MG1:2152907; Colec12.

Ensembl; ENSWUSGO000036103; Mus musculus.

MG2; G00.016020; C:imembrane; ISS.

G0; G00.016020; C:imembrane; ISS.

G0; G00.00016029; F:galactose binding; ISS.

RG; G0; 00016029; F:pattern recognition receptor activity; ISS.

RG; G0; 00019329; F:pattern recognition receptor activity; ISS.

RG; G0; 00019329; F:pattern recognition receptor activity; ISS.

RG; G0; 0001933; P:antibacterial humoral response (Bensu Vertebrata); ISS.

RG; G0; G0019734; P:antifungal humoral response (Bensu Vertebrata); ISS.

RG; G0; G0019734; P:innate immune response; ISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLECOTIDE SEQUENCE.

STRAIN=NMRI; TISSUE=Neammary tunnor. WAP-Tag model. 5 months old;
NUCLEOTIDE SEQUENCE.

MUCLEOLINE=22388257; PubMed=1247932; DOI=10.1073/pnas.245603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altachul S.F., Zeberg B. Buetow K.H., Schemen C.M., Schuler G.D.,
Altachul S.F., Zeberg B. B. Buetow K.H., Schemen C.M., Schuler G.D.,
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
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Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Ceneration and initial analysis of more than 15,000 full-length human
189 GPPGPPGPPGIPGIPGIPGTT-VMGPPGPPGPPGPPGPPGLQGPSGAADKAGTR--E 245
                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=NWRI; TISSUE-Mammary tumor. WAP-Tag model. 5 months old; Director MGC Project;
                                                                                                                                                                        246 NOPAV----VHLQGQGSAIQVKND----LSGGVLNDWSRITMNPKVF 284
                                                                                                                                                                                                                    Ohtani K., Sizuki Y., Eda S., Kawai T., Kase T., Keshi H.,
Fukuoh A., Sakamoto T., Itabe H., Suzutani T., Ogasawara M.
Yoshida I., Wakamiya N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yoshida I., Wakamiya N.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
10-MMY-2005 (TrEMBLrel. 30, Last annotation update)
Collectin placenta (Collectin sub-family member 12)
Name=Collectl; Synonyme=CL-Pl;
Mus musculus (Mouse).
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                742 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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Q8K4Q8;
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142 DEKPYSEEESRRVRRNKRSKSNEGADGPVKNKKKGKKAGPPGPNGPPGPPGP-----PG 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PQGPPGIPGI-----PGIPGTT-VMGPPGPPGPPGPQGPPGLQGPSGAADKAGTRENQP 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249 AVVHLQGQGSAIQVKKDLSGGVLNDWSRITMNPKVFKLHPRSGELEVLVDGTYFIYSQVE 308
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length
enriched library, clone:A730023E20 product:collectin sub-family member
12, full insert sequence.
R GO; GO:0045194; P:oxidized low-density lipoprotein catabolism; ISS.
R GO; GO:0006910; P:phagocytosis, recognition; ISS.
R GO; GO:001660; P:protein homocoligomerization; ISS.
R GO; GO:0044404; P:symbiotic interaction between host and othe. .; ISS.
R InterPro; IPR001363; Antifreezell.
R InterPro; IPR001360; Collagen.
R InterPro; IPR001391; Collagen.
R Pfam; PF00059; Lectin C; 1.
R Pfam; PF00059; Lectin C; 1.
R PROSITE; PS00615; C TYPE LECTIN 1; 1.
R ROSITE; PS00615; C TYPE LECTIN 1; 1.
R ROSITE; PS50041; C TYPE LECTIN 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        443 GPPGPRGPRGDRGSQGPPGP-TGNKGQKGEKGEPGPPGPA-----GERGTIGPVGPP
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Mammalia, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                                                                                                                                                                                                                                                                                                                            66; Gaps
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                                                                                                                                                                                                                                                                                                                                            13.4%; Score 282; DB 2; Length 742; 30.2%; Pred. No. 1.6e-08;
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Best Local Similarity 30.2%; Pred. No. 1.6e-us;
Bast Local Similarity 30.2%; Pred. No. 1.6e-us;
Matches 83; Conservative 29; Mismatches 97; Indels
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Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Puruno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchhonni L., Mashima J., Mazarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
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Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Subata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A., Yamamoto R., Matsumioto H., Sakaguchi S., Ikegami T., Kashivagi K., Yoneda Y., Ishikawa T., Casawa K., Izawa M., Ohara E., Watahiki M., Pujiwake S., Inoue K., Tozawa M., Ohara E., Watahiki M., Noneda Y., Ishikawa T., Ozawa K., Tanaka T., Haysahizaki Y., "RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Functional annotation of a full-length mouse cDNA collection.";
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GO; GO:0005737; C:Cytoplasm; IEA.
GO; GO:0005529; F:sugar binding; IEA.
GO; GO:0006817; P:phosphate transport; IEA.
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Pfam; PF00059; Lectin C; 1.
PRINTE; PR00356; ANTHEREZEII.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
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HSSP; P22897; 1EGI.
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InterPro, IPR008160, Collagen.
InterPro, IPR001304, Lectin_C.
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Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.

R EMBL; AB209864; BAD93101.1; -; mRNA.

R GO; GO:0005581; C:collagen; IEA.

GO; GO:0005737; C:cytoplasm; IEA.

R GO; GO:0005737; C:cytoplasm; IEA.

R GO; GO:0005715; P:cell adhesion; IEA.

R GO; GO:0005129; Featracellular matrix structural constituent; IEA.

R GO; GO:0005129; P:cell adhesion; IEA.

R InterPro; IPR001891; Collagen_C.

R InterPro; IPR001891; J. Laminin_G_TSP_N.

R Pfam; PF01410; COLFT; 1.

R Pfam; PF01410; COLFT; 1.

R R Pfam; PF01410; COLFT; 1.

R R MART; SM00028; LamG; 1.

R SMART; SM00210; TSPN; 1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                        494 GE------RGSKGSKGSKGSRGSPGKPGPQGPSGDPGPPGPPGKDGLPG
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                                                                                                                                                  443 GPPGPRGPKGDRGSQGPPGP-TGNKGOKGEKGEPGPPGPA------GERGTIGPVGPP
                                                                                                                                                                                    142 DEKPYSEEESRRVRRNKRSKSNEGADGPVKNKKKGKKAGPPGPNGPPGPPGP----PG
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Ohara O., Nagase T., Kikuno F.R.;
"None Title.";
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                                                  Length 742;
                                                Query Match
13.4%; Score 282; DB 2; Length 74;
Best Local Similarity 30.2%; Pred. No. 1.6e-08;
Matches 83; Conservative 29; Mismatches 97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1792 AA; 178517 MW; E47B3093C34C5A9D CRC64;
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SEQUENCE 742 AA; 91289 MW; 1350DCCB34522C45 CRC64;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                       309 VYYINPTDPASYEVVVDEKPPLQCTRSIETGKTNY 343
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10-MAY-2005 (TrEMBLrel. 30, Last sequence updaté
10-MAY-2005 (TrEMBLrel. 30, Last annotation upda
Pro-alpha-1 type V collagen variant (Fragment).
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TISSUE-Aorta endothelial cell;
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QS9EE7;
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NCBI_TaxID=9606;
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SEQUENCE
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae;
                                                                                                     132 OMALLINFFFDDEKPYSEEESRRVRRNKRSKSNEGADGPVKNKKKGKKAGPP---GPNGPP
                                                                                                                                           ------AGPPGERGPRGITGKPGPKGNSGGDGP-----AGPPGERGPNGPQ
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MEDLINE-90366601; PubMed-2203476; DOI=10.1016/0304-4165(90)90108-9;
Yaoi Y., Hashimoto K., Koltabashi H., Takahara K., Ito M., Kato I.;
Primary structure of the heparin-binding site of type V collagen.";
Bjochim. Biophys. Acta 1035:139-145(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       collagen alpha 1 (V) chain.";
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MEDLINE-94237164; PubMed-8181482;
Moradi-Ameli M., Rousseau J.C., Kleman J.P., Champliaud M.F.,
Boutillon M.M., Bernillon J., Wallach J.M., van der Rest M.;
Diversity in the processing events at the N-terminus of type-V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF 556-565.
MEDLINE=91302336; PubMed=2071595;
Takahara K., Seto Y., Okasawa K., Okamoto N., Noda A., Yaoi Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN SEQUENCE OF 565-576, 756-772; 1012-1029; 1219-1232 AND
                                                                                                                                                                              GPPGPPGPQGPPGIPGIPG-----TTVMGPPGPPGP------
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911 PLGPPGEKGKLGVPGLPGYPGRQGPKGS----IGFPGPP---
                                                                                                                                                                                                                                                                                       969 GHPGPPGPPGEQGLPGLAGKEGTK-GDPGPAGLPGK 1003
                                                                                                                                                                                                                                                      -- PGPOGPPGLOGPSGAADKAGTRENOPAVVHLOGO 256
                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 17, Created)
(Rel. 22, Last sequence update)
(Rel. 47, Last annotation update)
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Biol. Chem. Hoppe-Seyler 373:69-75(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete primary structure of human J. Biol. Chem. 266:13124-13129(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                        Collagen alpha 1(V) chain precursor. Name=COLSA1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bur. J. Biochem. 221:987-995(1994).
[6]
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MEDLINE=89227189; PubMed=2496661;
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                                                                         -GANGEKGGRGTP-----
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                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
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01-MAY-1992
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P20908;
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Interrupted collagenous region.

Triple-helical region.

Nonhelical region.

Sulforyrosine (Potential).

Sulforyrosine (Potential).
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Hydroxyproline.
5-hydroxylygine.
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  This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description; Collagen; Direct protein sequencing; Disease mutation; Ralers-Danlos syndrome; Extracellular matrix; Heparin-binding; Hydroxylation; Repeat; Signal; Structural protein; Sulfation.

1 37 Potential.

CHAIN 38 1605 Collagen alpha 1(V) chain.

PROPEP 1606 1838 C-terminal propeptide.

39 230 TSP N-terminal.
  DISEASE, AND VARIANT EDS-I SER-1639.
MEDLINE=97195540; PubMed=9042913;
de Paepe A., Nuytinck L., Hausser I., Anton-Lamprecht I.,
Naeyaert J.-M.;
"Muteations in the COL5A1 gene are causal in the Ehlers-Danlos syndromes I and II.";
Am. J. Hum. Genet. 60:547-554(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D90279; BAA14323.1; -; mRNA.
PDB; 1A89; Model; A/B/C=904-924.
PDB; 1A9A; Model; A/C=904-924.
Ensembl; ENSG00000130635; Homo sapiens.
HGNC; HGNC:2209; COL5Al.
MIM; 120215; -..
MIM; 130000; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0005589; C:collagen type V; TAS.
InterPro; IPR008161; Clg helix.
InterPro; IPR008161; Clg helix.
InterPro; IPR008161; Cladgen.
InterPro; IPR001815; Fib collagen.
InterPro; IPR001791; Laminin.G. TSP_N.
Pfam; PP01410; COLFI; I.
Pfam; PP01410; COLFI; I.
ProDom; PP000007; Clg_helix; 4.
ProDom; PP002078; Fib_collagen.C; I.
SWART; SM00282; LamG; 1.
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MEDLINE=92105142; PubMed=1722213;

A Greenspan D.S., Cheng W., Hoffman G.G.;

The pro-alpha 1(V) collagen chain. Complete primary structure,

I'm pro-alpha 1(V) collagen chain. Complete primary structure,

I'm collagen chain.";

J. Biol. Chem. 266:24727-24733(1991).

C. I- FUNCTION: May play an important role in fibrillogenesis by

C. I- SUBMONIT: Trimers composed of three different chains: alpha 1(XI),

alpha 2(XI), and alpha 3(XI). Alpha 3(XI) is a post-translational

modification of alpha 1(II). Alpha 1(V) can also be found instead

C. of alpha 3(XI)=1(II) (By similarity).

EMBL; W76729; AAA59993.1; -; mRNA.

PRESSIBELS CGMINGO.
                                                                                                                                                                                                                                                                                                                                                                    955 GPIGFPGPKGPPGPPGKDGLPGRGETGFQGKTGPPGPPGVKGPQGPTGETGPMGER 1014
                                                                                        10;
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                                                                                                                                                                                                                                                                    QMALLINFFFPDEKPYSEEESRRVRRNKRSKSNEGADGPVKNKKKGKKAGPP---GPNGPP 188
                                                                                                                                                                                                                                                                                                                                            189 GPPGPPGPQGPPGIPGIPG-----TTVMGPPGPPGP------ 222
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R GO; GO:0005581; C:cytoplasm; IEA.

R GO; GO:00057201; C:cytoplasm; IEA.

R GO; GO:0005201; F:extracellular matrix structural constituent; IEA.

R GO; GO:0005201; F:extracellular matrix

R GO; GO:0006817; P:potoplasm; IEA.

R GO; GO:0006817; P:potoplasm; IEA.

R InterPro; IPR0018161; Clg helix.

R InterPro; IPR001865; Fib collagen.

R InterPro; IPR001865; Fib collagen.

R InterPro; IPR001919; LamInin.G. TSP.N.

R Pfam; PP01391; COLE1; 1.

R Pfam; PP01391; COLE1; 1.

R Probom; PD002078; Fib_collagen.C; 1.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                         PAAAPRERGSQGC-GCGCAPARAGEGNSCLLFLGFFGLSLALHLLTLCCYLELRSELRRE
                                                                                                                                                                                               RGAESRIGGSGTPGTSGTLSSLGGLDPDSPITSHLGQPSPKQQPLEPGEAALHSDSQDGH
                                                                                                                                                                                                                                   892 -GANGEKGGRGTP------GKPGPRGQRGPTG-----
                                                                                        Gaps
                                                Score 280.5; DB 1; Length 1838;
Pred. No. 4.8e-08;
9; Mismatches 69; Indels 115;
                                                                                                                                                             857 PLGPPGEKGKLGVPGLPGYPGRQGPKGS----IGFPGFP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAX-2004 (TrEMBLrel. 26, Last annotation update)
Pro-alpha-i type V collagen.
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Hydroxyproline
Hydroxyproline
                                                    Query Match
Best Local Similarity 30.1%;
Matches 83; Conservative
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Q15094;
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NCBI_TaxID=9606;
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                                                                                            13.4%; Score 280.5; DB 2; Length 1838; 30.1%; Pred. No. 4.8e-08; indels 115; tive 9; Mismatches 69; Indels 115;
                                                                                                                                                                                      SMART; SM00038; COLFI; 1.
SMART; SM00282; LamG; 1.
SMART; SM00210; TSPN; 1.
Collagen; Extracellular matrix; Structural protein.
SEQUENCE 1838 Aa; 183612 MW; 5078307F6E00F0BA CRC64;
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; ORGANISM: Homo sapiens
US-09-342-681C-2
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2: /cgn2_6/ptodata/1/iaa/f_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                protein search, using sw model
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ALIGNMENTS

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JOS-09-3-12-001.2-5

Sequence 2, Application US/09342681C

Patent No. 6355782

GENERAL INFORMATION:

JAPLICANT: Zonana et al.

TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins

FILE REFERENCE: 52978

CURRENT APPLICATION NUMBER: US/09/342,681C

CURRENT PILING DATE: 1998-06-29

PRIOR APPLICATION NUMBER: 60/092,79

PRIOR APPLICATION NUMBER: 60/112,366

PRIOR FILING DATE: 1998-12-15

NUMBER OF SEQ ID NOS: 123

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2

LENGTH: 391
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100.0%; Pred. No. 1.4e-168;
ive 0; Mismatches 0;
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TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
TITLE OF INVENTION: 1999-106-29
CURRENT APPLICATION NUMBER: 00/092,279
PRIOR FILING DATE: 1998-07-09
PRIOR FILING DATE: 1998-07-09
PRIOR FILING DATE: 1998-07-01
PRIOR FILING DATE: 1998-12-15
NUMBER OF SEQ ID NOS: 123
SOFTWARE: Patentin Ver. 2.1
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100.0%; Pred. No. 1.4e-168;
tive 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FBSESEQ for Windows Version 4.0
SEQ ID NO 6074
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                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                          ) ORGANISM: Human
US-09-949-016-6074
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Best Local Simil
Matches 391; (
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Patent No. 6812339
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
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                                                                                                                                        Sequence 6, Application US/10012605C

Patent No. 6692748

GENERAL INFORMATION:
APPLICANT: Haldeman, Betty A.
APPLICANT: Thayer, Edward C.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: ADIPOCYTE COMPLEMENT RELATED PROTEIN
TITLE OF INVENTION: ADIPOCYTE COMPLEMENT RELATED PROTEIN
TITLE OF INVENTION: ADIPOCYTE COMPLEMENT RELATED PROTEIN
GURRENT APPLICATION NUMBER: US/10/012,605C
CURRENT FILING DATE: 2002-08-14
PRIOR PILING DATE: 2002-08-14
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 2098; DB 2; Best Local Similarity 100.0%; Pred. No. 1.4e-168; Matches 391; Conservative 0; Mismatches 0;
                                361 AVKMVHADISINMSKHTTFFGAIRLGEAPAS 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-605C-6
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                                                                                                                                                                                                                                                                                                                                                                                B: Flehr, Hobbach, Test, Albritton & Herbert
Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: VC-JUS, MS-LUS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/609,716
FILING DATE: 06-NOV-1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20015
REFRENCE/DOCKET NUMBER: 20015
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1000 66:
SEQUENCE CHRAACTERISTICS:
LENGTH: 357 amino acids
                                                                                                                                                   Sequence 66, Application US/07609716
; Sequence 80. 5514581
; Fatent No. 5514581
; GENERAL INFORMATION:
APPLICANT: Cappello, Joseph
TITLE OF INVENTION: Functional Recombinantly Preg
TITLE OF INVENTION: Synthetic Protein Polymer
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & He
STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213 -VMGPPGPPGPPGPQGPPGLQGPSGAADKAGTR 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189 GPPGPPGPQGPPGIPGIPGTT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 33, Application US/08642255; Parent No. 5773249; GENERAL INFORMATION:
                           241 NMSKHTTFFGAIRLGEAPAS 260
372 NMSKHTTFFGAIRLGEAPAS 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 32.4 Matches 69; Conservative
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US-08-642-255-33
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                                                                                                                       RESULT 6
US-07-609-716-66
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Sequence 11119, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERRENCE: CL001307

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR PLING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOOTHARE: PaatSEQ for Windows Version 4.0

SEQ ID NO 11119
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                                                                          61 YLELRSELRRERGAESRIGGSGTPGTSGTLSSLGGLDPDSPITSHIGQPSPKQQPLEPGE 120
                                                                                                           121 AALHSDSQDGHQMALLINFFFPDEKPYSEEESRRVRRNKRSKSNEGADGPVKNKKKGKKAG 180
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301 YFIYSQVEVYYINFTDFASYEVVVDBKPFLQCTRSIBTGKTNYNTCYTAGVCLLKARQKI
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Best Local Similarity 100.0%; Pred. No. 2.9e-110;
Matches 260; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 AVYMVHADISINMSKHTTFFGAIRLGEAPAS 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             347 AVKMVHADISINMSKHTTFFGAIRLGEAPAS 377
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US-09-949-016-11119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 D---------RGDAGPKGADGSPGPAGPVGSPGAPGPPGPPGPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
14.0%; Score 294; DB 1; Length 357;
Best Local Similarity 32.4%; Pred. No. 1.1e-16;
Matches 69; Conservative 9; Mismatches 71; Indels 64; Gaps
                                                                                                                       NUMBER OF SEQUENCES: 135

CORRESPONDENCE ADDRESS:
ADDRESSE: FLERH, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-475-411A-66

Sequence 66, Application US/08475411A
Sequence 66, Application US/08475411A
Sequence 66, Application US/08475411A
SENERAL INFORMATION:
APPLICANT: Ferrari, Franco A.
APPLICANT: Cappello, Joseph
TILLE OF INVENTION: Synthetic Protein Polymer
NUMBER OF INVENTION: Synthetic Protein Polymer
CORRESPONDENCES: 119
CORRESPONDENCES: 119
CORRESPONDENCES: 119
STREET: Four Embarcadero Center, Suite 3400
APPLICANT: CAPPELLO, Joseph
APPLICANT: FERRARI, Franco A.
TITLE OF INVENTION: High Molecular Weight Collagen-Like
TITLE OF INVENTION: Protein Polymers
TITLE OF INVENTION: 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSEE: Flehr, Hohbach, Test, Albritton & Herbert
T: Four Embarcadero Center, Suite 3400
San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/642,255 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    226 GPPGAPGPPGPPGPPGLPGPKGDRGDAGPK 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, BERTERAIL
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A5556-3/BIR
TELEPHONE: (415) 494-870
TELEPHONE: (415) 494-871
TELEPAX: (415) 494-877
TELERA: (415) 494-877
TELEC : 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 GPPGPPGPPGIPGIPGIT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-642-255-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
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71 ERGAESRIGGSGTPGTSGTLSSLGGLDPDSP--ITSHLGOPSPKQOPLBPGEAALHSDSQ 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 DGHQMALLNFFFPDEKPYSEEESRRVRRNKRSKSNEGADGPVKNKKKGKKAGPPGPNGPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 DRGDAGPKGADGSPGPAGPVGSPGAPGPPGPPGAPGPPGAPGPPGPPGPPGPPGPPGPPGPKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64; Gaps
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                                                                                                    CURRENT APPLICATION DATA:

SOFTWARE Patentin Release #1.0, Vergion #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/475,411A

FILING DATE: 07-JUN-1995

RIOR APPLICATION NUMBER: US 07/609,716

PRIOR APPLICATION NUMBER: US 07/609,716

PRIOR APPLICATION NUMBER: US 07/269,429

FILING DATE: 06-NOV-1990

PRIOR APPLICATION NUMBER: US 07/269,429

FILING DATE: 09-NOV-1986

RIOR APPLICATION NUMBER: US 07/114,618

APPLICATION NUMBER: US 07/114,618

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 06/927,258

FILING DATE: 03-OCT-1987

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 06/927,258

FILING DATE: 04-NOV-1986

ATTONEY/AGRET INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 294, DB 2;
Pred. No. 1.1e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213 -VMGPPGPPGPPGPQGPPGLOGPSGAADKAGTR 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   226 GPPGAPGPPGPPGPPGLPGPKGDRGDAGPK 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REPERDICE/DOCKET NUMBER: A-55186-9/RFT/WIX
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEPHONE: 415-384-3249
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189 GPPGPPGPPGIPGIPGIPGTT-----
                                                                                      PC-DOS/MS-DOS
                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 32.4%;
Matches 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          357 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-08-475-411A-66
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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79 GGSGTPGTSGTLSSLGGLDPDSPITSHLGQPSPKQQPLEPGBAALHSDSQDGHQMALLNP 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 FPPDEKPYSERESRRVRRNKRSKSNEGADGPVKNKKKKKKAGPPGPNGPPGPPGPPGPQG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 GPPGPPGPAGPVGSPGAPGPPGP----PGPPGPPGAPGPPG---------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 277; DB 1; Length 330;
Pred. No. 2.7e-15;
5; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 199 PPGIPGIPGIPGTTVMGPPGPPGPPGPQGPPGLQGPSGAADKAGT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 PVGSPGAPGPPGPP--GPPGPPGAPGPPGPPGPPGPPGPAGPVGS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSEE: Flehr, Hobbach, Test, Albritton & Herbert
F: Four Embarcadero Center, Suite 3400
San Prancisco
               ADDRESSER: FLERK, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco CITY: San Francisco CITY: Sal Francisco COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 65, Application US/07609716
Patent No. 5514581
GENERAL INFORMATION:
APPLICANT: Cappello, Joseph
TITLE OF INVENTION: Functional Recombinantly Prepared
TITLE OF INVENTION: Synthetic Protein Polymer
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,255
                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FOWLAND, Bertram I.
REJESTRATION NUMBER: 20,015
REPERENCE/DOCKET NUMBER: A55556-3/BIR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 13.2%;
Best Local Similarity 39.4%;
Matches 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 330 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / MOLECULE TYPE: protein US-08-642-255-32
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                   FILING DATE:
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US-07-609-716-65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 DGHQMALLINFFFPDEKPYSEEESRRVRRNKRSKSNEGADGPVKNKKKKKKKGKKAGPPGPNGPP 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166 GPPGAPGPPGPPGPPGLPGPKGDRGDAGPKGADGSPGPAGPVGSPGAPGPPGPP 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
14.0%; Score 294; DB 2; Length 357;
Best Local Similarity 32.4%; Pred. No. 1.1e-16;
Matches 69; Conservative 9; Mismatches 71; Indels 64; Gaps
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Sequence 32, Application US/08642255

Patent No. 5773249

GENERAL INFORMATION:

APPLICANT: CAPPELLO, Joseph

APPLICANT: FERRARI, Franco A.

TITLE OF INVENTION: High Molecular Weight Collagen-Like

TITLE OF INVENTION: Protein Polymers

NUMBER OF SEQUENCES: 135
                                                                                   CUMPLAIR: C.
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURSTING DATE: 07-UNA-1995
CLIASSIFICATION NUMBER: US/08/478,029A
FILING DATE: 07-UNA-1995
CLIASSIFICATION NUMBER: US 07/609,716
FILING DATE: 06-NOV-1990
PRIOR APPLICATION NUMBER: US 07/269,429
FILING DATE: 09-NOV-1988
PRIOR APPLICATION NUMBER: US 07/114,618
FILING DATE: 29-OCT-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/927,258
FILING DATE: 129-OCT-1987
PRIOR APPLICATION NUMBER: 31,801
REGISTRATION NUMBER: 31,801
RELEPAN: 415-389-3249
INFORMATION POR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
'-RANGTH: 357 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226 GPPGAPGPPGPPGPPGLPGPKGDRGDAGPK 258
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     STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 GPPGPPGPPGIPGIPGIT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 357 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-478-029A-66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 FFPDEKPYSEEESRRVRRNKRSKSNEGADGPVKNKKKGKKAGPPGPNGPPGPPGPPGPQG 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 GPPGPPGPAGPVGSPGAPGPPGP----PGPPGPPGAPGPPG------94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
13.2%; Score 277; DB 1; Length 408;
Best Local Similarity 39.4%; Pred. No. 3.5e-15;
Matches 65; Conservative 5; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-475-411A-65
; Sequence 65, Application US/08475411A
; Sequence 65, Application US/08475411A
; Sequence 65, Application US/08475411A
; GENERAL INFORMATION:
; APPLICANT: Perrari, Franco A.
; TITLE OF INVENTION: Synthetic Protein Polymer
; TITLE OF INVENTION: Synthetic Protein Polymer
; NUMBER OF SEQUENCES: 119
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Pour Embarcadero Center, Suite 3400
; CITY: San Francisco
; STREET: CAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 199 PPGIPGIPGIPGTTVMGPPGPPGPPGPQGPPGLQGPSGAADKAGT 243
146 PVGSPGAPGPPGPPG-GPPGPPGPPGPPGPPGPPGPPGPPGPPGP 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILING DATE: 07-JUN-1995
                                                                                                                                                                      A-55186-3/BIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/609,716
FILING DATE: 06-NOV-1990
PRIOR APPLICATION NUMBER: US 07/269,429
FILING DATE: 09-NOV-1988
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/114,618
FILING DATE: 29-OCT-1987
FILING DATE: 29-OCT-1987
FILING DATE: 29-OCT-1987
APPLICATION NUMBER: US/07/609,716
FILING DATE: 06-NOV-1990
CLASSIFTCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A-55186-3/B
TELEFAN: 415-781-1989
TELEFAN: 415-781-1989
TELEFAN: 415-39-3249
TELEFAN: 415-39-3249
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 408 amino acide
TYPE: amino acid
TYPE: amino acid
TYPE: amino acide
TYPE: amino acide
TYPE: amino acide
TYPE: amino acide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ઠ
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PILLING DATE: 04-NOV-1986

ATTORNEY/AGENT INPORMATION:

RESTERRENEY/AGENT INPORMATION:

RESTERRATOR WHERE: 13.101

RESTERRATION TO SEND THOUGHT INPORMATION: 10.001

RESTERRATION TO SEND THOUGHT INPORMATION: 10.001

RESTERRATION TO SEND THOUGHT INPORMATION: 10.001

RESTERRATION TO SEND THOUGHT INPORMATION: 13.001

RESTERRATION TO SEND THOUGHT INPORTED THOUGHT IN THOUGHT INPORTATION TO SEND THOUGHT INPORTATION TO SEND THOUGHT IN T
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                                                     ------PPGADGQPGAKGEPGDAGAKGDAGPPGPAGP----AGPPGPIGNVGAPGA- 700
                                                                                                                                      ------KGARGSAGPPGATGFPGAAGRVGP 724
                                                                                                                                                                              PGPNGPPGPPGP-----QGPPGIPGIPGIPGITVWGPPGPPGPPGPQGPPGLQGPS 235
                                                                                                                                                                                                   13 PAAAPRERGSOG-----CGCGGAPARAGE----GNSCLLFLGFFGLSLALHLLTLCCY
                 LELRSELRRERGAESRIGGSGTPGTSGTLSSIGGLDPDSPITSHIGQPSPKQQPLEPGEA
                                                                                               122 ALHSDSQDGHQMALLINFPFPDEKPYSEESRRVRRNKRSKSNEGADGPVKNKKKGKKAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1057;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: GRUSKIN, ELLIOT A.
BUECHTER, DOUGLAS
BROKAN, JANBE
ZHANG, GUANGHUI
PAOLELLA, DAVID
TITLE OF INVENTION: AMINO ACID MODIFIED POLYPEPTIDES
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/153,469A
FILING DATE: 22-May-2002
CLASSIPICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.7%; Score 265.5; DB 2;
29.7%; Pred. No. 1.1e-13;
tive 16; Mismatches 80;
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STREET: 333 EARLE OVINGTON BOULEVARD
CITY: UNIONDALE
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APPLICATION NUMBER: US/09/169,768
FILING DATE: 09-OCT-1998
ATTORNEY/AGENT INFORMATION:
NAME: STEEN, JEFFREY S
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 228-6894
TELEFRAX: (516) 228-8516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown MOLECULE TYPE: peptide ; SEQUENCE DESCRIPTION: SEQ ID NO: 16: US-10-153-469A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                               GAADKAGTR--ENQPAVVHLQGQ 256
                                                                                                                                                                                                                                                                                                       783 GAPGTPGPQGIAGÓRGVVGLPGÓ 805
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; Sequence 16, Application US/10153469A
; Patent No. 6927287
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 PFPDEKPYSEEESRRVRRNKRSKSNEGADGPVKNKKKGKKAGPPGPNGPPGPPGPQG 198
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                                                                                                                                                                                                                                                                                                       Query Match
13.2%; Score 277; DB 2; Length 408;
Best Local Similarity 39.4%; Pred. No. 3.5e-15;
Matches 65; Conservative 5; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            199 PPGIPGIPGIPGTTVMGPPGPPGPPGPQGPPGLQGPSGADKAGT 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/931,820
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Assay for collagen degradation NUMBER OF SEQUENCES: 4
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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NAME: Trecartin, Richard F.
REGISTRATION VMDBER: 31,801
REFERENCE FOOCKET NUMBER: 4.55186-8/RFT/MTK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEPAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 4008 amino acide
TYPE: amino acid
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 96202596.1
FILING DATE:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1057 amino acids
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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MOLECULE TYPE: protein
                                                                                                                                                                                                            single
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Matches 78; Conserv
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TISSUE TYPE:
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US-08-931-820-1
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ò	182 PGE	PGPNGPPGPPGPPGPQGPPGIPGIPGTTVMGPPGPPGPPQPPGGPPGLQGPS 235
qa	725 PGI	PGPSGNAGPPGPPGPPGKEGGKGPRGETGPAGRPGEVGPPGPPGPPGBAGKGSPGADGPA 782
Š	236 GAJ	236 GAADKAGTRENQPAVVHLQGQ 256
qa	783 GA	
Search Job tim	Search completed: Job time : 24 secs	Search completed: January 13, 2006, 16:15:56 Job time : 24 Becs

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Sequence 2, Appli
Sequence 42, Appli
Sequence 6, Appli
Sequence 46, Appli
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Sequence 6
Sequence 9
Sequence 8
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Sequence 4
Sequence 3
Sequence 5
Sequence 5
Sequence 6
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1 MGYPEVERRELLPAAAPRER......NMSKHTTFFGAIRLGEAPAS
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/cgn2 6/ptcdata/1/pubpa/USO8 PUBCOMB.pep:*
/cgn2 6/ptcdata/1/pubpa/USO8 PUBCOMB.pep:*
/cgn2 6/ptcdata/1/pubpaa/USO8 PUBCOMB.pep:*
/cgn2 6/ptcdata/1/pubpaa/USIOB_PUBCOMB.pep:*
/cgn2 6/ptcdata/1/pubpaa/USIOB_PUBCOMB.pep:*
GenCore version 5.1.6 (c) 1993 - 2006 Compugen Ltd.
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US-09-729-658B-2

US-10-112-652-4

US-10-310-793-46

US-10-310-793-46

US-10-202-062-42

US-10-202-062-42

US-10-119-205-6

US-11-142-736-9

US-11-142-736-9

US-10-503-999-6

US-10-503-999-6

US-10-503-999-6

US-10-503-999-6

US-10-185-425-9

US-10-185-425-9

US-10-185-425-9

US-10-185-425-9

US-10-185-2

US-10-185-2

US-10-820-155-2

US-10-820-155-2

US-10-820-155-2

US-10-820-155-2

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Maximum Match 100%
Listing first 45 summaries
                                                                                              - protein search, using sw model
                                                                                                                                            January 13, 2006, 16:15:03
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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	S Drosophila Tumor Necrosis	Drosophila melanogaster 100.0%; Score 2098; DB 3; Length 391; imilarity 100.0%; Pred. No. 2.6e-137; Conservative 0; Mismatches 0; Indels 0; Gaps MGYPEVERRELLPAAAPRERGSQGGGGGAPARAGEGNSCLLFLGFFGLSLALHLLTLCC
US-10-402-072A-4 US-10-402-072A-6 US-10-901-816A-10 US-10-203-860-2 US-10-820-155-8 US-10-820-155-8 US-10-820-155-17 US-10-223-084-28 US-10-223-084-28 US-10-223-084-28 US-10-223-083-28	dos	Drosophila melanogaster 100.0%; Score 2088; DB 3; imilarity 100.0%; Pred. No. 2.6e-137; Conservative 0; Mismatches 0; MGYPEVERRELLPAAAPRERGSGGGGGAPARAGEGNS
402-072A-4 402-072A-6 901-072A-6 901-072A-6 913-08-08-08-08-08-08-08-08-08-08-08-08-08-	Dro	9; 2.6 2.6 PARA PARA PARA PARA PARA SSLG SSLG SSLG FILL
0000 0000 0100	ALIGNMENT 9 72966Alel reof /813,329	ore 2098; ed. No. 2. Mismatches GCGCGGAPAR GCGCGGAPAR HTH
00000000000000000000000000000000000000	LIGN pany 968A eof 813,	Score Pred. Mism SQCGC SQCGC GTPGTS G
0.5-10-46 (Al 329 (122) (123)	Score Pred // Mil // Mil // SSOCC GSOCC GS
4 4 72 4 4 72 72 4 4 4 4 4 4 4 4 4 4 4 4	ALIGNMEN ULT 1 09-813-329-8 equence 8, Application US/09813329 equence 8, Application US/09813329 extent No. US20020012968A1 ENERAL INFORMATION: APPLICANT: Briscol-Myers Suibb Company TITLE OF INVENTION: No. US20020012968A1e1 TITLE OF INVENTION: No. US20020012968A1e1 TITLE OF INVENTION: No. US20020012968A1e1 FILE REFREENCE: D0016.np CURRENT FILING DATE: 2001-03-20 PRIOR PILING DATE: 2000-03-21 SOFTWARE: PACENTIN NOWBER: 60/190,816 BRIOR FILING DATE: 2000-03-21 SOFTWARE: PACENTIN VERSION 3.0 EQ ID NO 8 EMENCH: 391 TWOR: PRT	Drosophila melanogaster 100.0%; Score 2098 100.0%; Pred. No ; Conservative 0; Mismatch MGYPEVERRELLPAAAPRERGSQGGGGGAP
	S/03 1 Su; Su; iant iant iant oo; 603-603-7	100.0%; 100.0%; 100.0%; 1ve PAAAPREJ PAAAPREJ GAESRLGG H
10466 10467 10467 10467 10467 10468	1-329-8 1e 8, Application US/ No. US20020012968A1 1. INFORMATION: No. US OF INVENTION: TAPPLICATION NUMBER: TAPPLICATION NUMBER: TAPPLICATION NUMBER: TAPPLICATION NUMBER: TAPPLICATION NUMBER: TOO DE SEQ ID NOS: 65 NO 8 NO 8 HE: 991 PRET	BODHILA MELA 100 CONSERVATIVE 100 CONSERVATIVE 100 PEVERRELLPAA LRSELRREGAE LRSELRREGAE LRSELRREGAE LRSELRREGAE LRSELRERGAE LRSELRERGA
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	SULT 1 -09-813-329-8 Sequence 8, Application US Sequence 10, Application US BREATH NO. US20020012968A; APPLICANT: Bristol-Myers TITLE OF INVENTION: No. UTITLE OF INVENTION: No. UTITLE OF INVENTION: No. UTITLE OF INVENTION: NATIVE OF INVENTION: NATIVE OF INVENTION: NATIVE OF INTING DATE: 200 PRIOR FILING DATE: 200 PRIOR FILING DATE: 2000-0 SOFTWARE: PATENTING DATE: 2000-0 SOFTWARE: PATENTING DATE: 2000-0 SEQ ID NO 8 SEQ ID NO 8 ERNOR: BERTHER INVENTION: SES SOFTWARE: PATENTING DATE: 2000-0 SERVING APPLICATION NUMBER: PATE	18
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Best Local Similarity 100.0%; Score 2098; DB 4; Length 391;
Best Local Similarity 100.0%; Pred. No. 2.6e-137;
Matches 391; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                              100.0%; Score 2098; DB 4; Length 391; 100.0%; Pred. No. 2.6e-137;
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GENERAL INFORMATION:
APPLICANT: Haldeman, Betty A.
APPLICANT: Thaper, Edward C.
APPLICANT: Thaper, Edward C.
TITLE OF INVENTION: ADIPOCYPE COMPLEMENT RELATED PROTEIN
TITLE OF INVENTION: ADIPOCYPE COMPLEMENT RELATED PROTEIN
TITLE OF INVENTION: ADIPOCYPE COMPLEMENT RELATED PROTEIN
CURRENT PAPLICATION NUMBER: US/10/012,605C
CURRENT FILING DATE: 2002-08-14
PRIOR PLILING DATE: 2000-12-07
PRIOR PLILING DATE: 2000-12-07
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SOFTWARE: FastSEQ for Windows Version 4.0
PRIOR FILING DATE: 2001-08-16
PRIOR APPLICATION NUMBER: 60/330,761
PRIOR FILING DATE: 2001-10-30
NUMBER OF SEQ ID NOS: 57
SOFTWARE: Patentin version 3.1
LENGTH: 391
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Best Local Similarity 100.
Matches 391; Conservative
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US-10-012-605C-6
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                                                                                                                                                                                  Sequence 2, Application US/09729658B

; Sequence 2, Application No. US20030023991A1
; Publication No. US20030023991A1
; GENERAL INPORMATION:
    APPLICAWT: Zonana et al.
    TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
    TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
    TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
    TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
    FILE REPERENCE: 55924
    CURRENT APPLICATION NUMBER: 09/342,681
    PRIOR PILING DATE: 1999-06-29
    PRIOR PILING DATE: 1999-06-29
    PRIOR PILING DATE: 1999-06-29
    PRIOR APPLICATION NUMBER: 60/12,366
    PRIOR APPLICATION NUMBER: 60/112,366
    NUMBER OF SEQ ID NOS: 122
    SOFTWARE: Patentin Ver. 2.1
    TENGRAL SEQ ID NO 2.
    TENGRAL SEQ ID NO 2.
    TENGRAL SEQ ID NO 2.
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Matches 391; Conservative 0; Mismatches 0; Indels 0
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US-10-218-547-42
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Sequence 42, Application Ws/10202062

Publication No. US20040038349A1

GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc.,

TILLE OF INVENTION: Heteromultimeric TNF Ligand Family members

PILE REFERENCE: PFS59

CURRENT PILING DATE: 2002-07-25

PRIOR PILING DATE: 2001-07-27

NUMBER OF SEQ ID NOS: 42

SOFTWARE: Patentin version 3.0

SEQ ID NO 42

LENGTH: 391
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  0; Mismatches
  Matches 391; Conservative
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US-10-202-062-42
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Pred. No. 2.6e-137;
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241 AGTRENQPAVVHLQGQGSAIQVKNDLSGGVLNDWSRITMNPKVFKLHPRSGELEVLVDGT 300
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                                                             YFIYSQVEVYYINPTDFASYEVVVDEKPFLQCTRSIETGKTNYNTCYTAGVCLLKARQKI
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APPLICANT: Haldeman, Betty A.
APPLICANT: Thayer, Edward C.
APPLICANT: Thayer, Edward C.
APPLICANT: Theoreman Sheppard, Paul O.
TITLE OF INVENTION: ADPROCYTE COMPLEMENT RELATED PROTEIN
TITLE OF INVENTION: ZACRP3X2
FILE REFERENCE: 00-111
CURRENT APPLICATION NUMBER: US/10/719,205
CURRENT FILING DATE: 2003-11-21
PRIOR APPLICATION NUMBER: US/00/012,605C
PRIOR PLILING DATE: 2003-01-4
PRIOR FILING DATE: 2003-01-4
PRIOR FILING DATE: 2003-01-4
PRIOR FILING DATE: 2003-01-4
SPRIOR FILING DATE: 2003-11-207
SPRIOR PRIOR P
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Pred. No. 2.6e-137;
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Publication No. US20040086971A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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RESULT 8 US-11-028-780-42 Sequence 42, Application US/11028780 ; Publication No. US20050163747A1

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Sequence 8, Application US/11142736

Publication No. US20050227283A1

GENERAL INFORMATION:

TITLE OF INVENTION: Novel Drosophila Tumor Necrosis Factor Class Molecule ("DMTNF") a

TITLE OF INVENTION: Variants Thereof

FILE REFERENCE: D0016 D1V1

CURRENT FILING DATE: 2005-06-01

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-03-21
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APPLICANT: Human Genome Sciences, Inc.,
TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members
FILE REFERENCE: PF559C1
CURRENT APPLICATION NUMBER: US/11/028,780
CURRENT FILING DATE: 2005-01-05
PRIOR FILING DATE: 2002-07-25
PRIOR FILING DATE: 2001-07-25
PRIOR FILING DATE: 2001-07-27
NUMBER OF SEQ ID NOS: 42
SOFFWARE: Patentin version 3.2
SEQ ID NO 42
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ORGANISM: Drosophila melanogaster
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SOFTWARE: Patentin version 3.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 391; Conservative
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Sequence 9, Application US/11142736
Publication No. US20050227283A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Suibb Company
TITLE OF INVENTION: Novel Drosophila Tumor Necrosis Factor Class Molecule ("DmTNF")
TITLE OF INVENTION: UNMERS: US/11/142,736
CURRENT APPLICATION UNMERS: 06/190,816
PRIOR APPLICATION NUMBER: 60/190,816
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
SOFTWARE: Patentin version 3.0
SEQID NOS: 65
SEQID NOS: 65
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AGTRENQPAVVHLQGQGSAIQVKNDLSGGVLNDWSRITMNPKVFKLHPRSGELEVLVDGT
                   241 TGTRENQPAVVHLQGQGSAIQVKNDLSGGVLNDWSRITMNPKVFKLHPRSGELEVLVDGT
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Pred. No. 4.3e-128;
1; Mismatches 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 93.7%;
Best Local Similarity 94.6%;
Matchee 370; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Mus musculus US-11-142-736-9
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US-09-729-658B-4
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TYPE: PRT
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US-11-142-736-9
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Setent No. US2002012968A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL BETISTOI-Myers Suibb Company
TITLE OF INVENTION: No. US20020012968A1e1 Drosophila Tumor Necrosis Factor Class Mole
TITLE OF INVENTION: Variants Thereof
FILE REFERENCE: D0016.mp
CURRENT APPLICATION NUMBER: US/09/813,329
CURRENT FILING DATE: 2001-03-20
PRIOR APPLICATION NUMBER: 60/190,816
FRIOR RILING DATE: 2000-03-21
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9
LENGTH: 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGGPNGPPGPPGPPGPPGIPGIPGIPGIPGTTVMGPPGPPGPPGPPGPPGPGGPPGADADK 240
                                                                                                                                                     61 YLELRSELRRERGAESRLGGSGTPGTLSSLGGLDPDSPITSHLGQPSPKQQPLEPGE 120
                                                                                                                                                                                                                        PPGPNGPPGPPGPPGPPGIPGIPGIPGITVMGPPGPPGPPGPPGPPGGPPGLQGPSGAADK 240
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                                                                                                                                                                                                     121 AALHSDSQDGHQMALLNPFFPDEKPYSEEBSRRVRRNKRSKSNEGADGPVKNKKKGKKAG 180
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                                                                                1 MGYPBVERRELLPAAAPRERGSQGCGCGGAPARAGEGNSCLLFLGFFGLSLALHLLTLCC
                                                                                                                                                                                                                                                                                                                                                                            241 AGTRENQPAVVHLQGQGSAIQVKNDLSGGVLNDWSRITWNPKVPKLHPRSGBLBVLVDGT
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                                                                                                                              61 YLELRSELRRERGAESRIGGSGTPGTSGTLSSIGGLDPDSPITSHLGQPSPKQQPLEPGE
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                   Indels
 Local Similarity 100.0%; Pred. No. 2.6e-137; Nes 391; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1965; DB 3;
Pred. No. 4.3e-128;
1; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 AVKMVHADISINMSKHTTFFGAIRLGEAPAS 391
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Best Local Similarity 94.6%;
Matches 370; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Mus musculus
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US-09-813-329-9
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Length 412; 15; Indels

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Sequence 8, Application US/10503999;
Sequence 8, Application No. US20050152872A1

Bublication No. US20050152872A1

GENERAL INPORMATION:
APPLICANT: Gaide, Olivier
APPLICANT: Schneider, Pascal
APPLICANT: Schneider, Pascal
APPLICANT: Tachopp, Jurg
TITLE OF INVENTION: Fusion Constructs Containing Active Sections Of TNF Ligands
TITLE OF INVENTION: Fusion Constructs
CURRENT APPLICATION NUMBER: US/10/503,999
CURRENT FILING DATE: 2004-08-09
PRIOR PELICATION NUMBER: DE 102 05 368.5
PRIOR APPLICATION NUMBER: DE 102 05 368.5
PRIOR PELING DATE: 2002-02-10

PRIOR FILING DATE: 2002-02-11

PRIOR FILING DATE: 2002-02-12

PRIOR FILING DATE: 2002-02-13

FRIOR FILING DATE: 2002-02-13

FRIOR SEQ ID NOS: 22

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin version 3.2

SEQ ID NO 8

SEQ ID NO 8

SEX ID NO 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         275 SRITMNPKVFKLHPRSGELEVLVDGTYFIYSQVEVYYINFTDFASYEVVVDEKPFLQCTR 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              296 SRITMNPKVFKLHPRSGELEVLVDGTYFIXSQ--VYXINFTDFASYEVVVDEKPFLQCTR 353
                                                                                                                                                                                                                                                       242 GKRSPQPQPKPQPKP---EPEGSLQ----VDENQPAVVHLGGGGSAIQVKNDLSGGVLNDW 295
                                                                                                                                                                                                                                                                                                           SRITMNPKVFKLHPRSGELEVLVDGTYPIYSQVEVYYINFTDFASYEVVVDEKPFLQCTR 334
                                                                                                                                                                                                                                                                                                                                       296 SRITMNPKVFKLHPRSGELEVLVDGTYFIXSQVEVYXINFTDFASYEVVVDEKPFLQCTR 355
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                                                                                                                                                                                                                                                                                                                                                                                                    335 SIETGKTNYNTCYTAGVCLLKARQKIAVKMVHADISINMSKHTTFFGAIRLGEAPAS 391
                                                                                                                                                                                                                                                                                                                                                                                                                            356 SIETGKTNYNTCYTAGVCLLKARQKIAVKOVHADISINMSKHTTFFGAIRLGEAPAS 412
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                                                                                                                                                                                                                    215 GPPGPPGPPGPPGLQGPSGAADKAGTRENQPAVVHLQGQGSAIQVKNDLSGGVLNDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 759; DB 5; Length 410;
Pred. No. 1.9e-44;
1; Mismatches 15; Indels
                                                                                                                               Query Match
37.1%; Score 779; DB 5;
Best Local Similarity 87.6%; Pred. No. 7.9e-46;
Matches 155; Conservative 1; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , OTHER INFORMATION: Synthetic Construct US-10-503-999-8
; TYPE: PRT
; ORGANISM: artificial
; PEATURN: NPORMATION: Synthetic Construct
US-10-503-999-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence 9, Application US/10185425; Publication No. US20030053984A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 86.4%;
Matches 153; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
US-10-185-425-9
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Sequence 6, Application US/10503999;
Publication No. US20050152872A1
GENERAL INFORMATION:
APPLICANT: Gaide, Olivier
APPLICANT: Schneider, Pascal
APPLICANT: Tschopp, Jurg
TITLE OF INVENTION: Fuelon Constructs Containing Active Sections Of TNF Ligands
FILE REFERENCE: 11436*13
CURRENT APPLICATION NUMBER: US/10/503,999
CURRENT FILING DATE: 2004-08-21
FRIOR PILING DATE: 2002-08-21
FRIOR FILING DATE: 2002-02-10
FRIOR PELICATION NUMBER: DE 102 05 368.5
FRIOR FILING DATE: 2002-02-10
FRIOR APPLICATION NUMBER: DE 102 05 583.1
FRIOR FILING DATE: 2002-02-11
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.2
SEQ ID NO 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            294 -----EVYYINFTDFASYEVVVDEKPFLQCTRSIETGKTNYNTCYTAGVCLLKARQKI 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MGYPEVERRELLPAAAPRERGSQGCGCGGAPARAGEGNSCLLFLGFFGLSLALHLLTLCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14;
                                                                                                                                                                                                                                                                                                                                                                                                                   89.3%; Score 1873; DB 3; Length 377; 90.8%; Pred. No. 1e-121; tive 2; Mismatches 20; Indels 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 AVKWVHADISINMSKHTTFFGAIRLGEAPAS 391
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CURRENT APPLICATION NUMBER: US/09/729,658B
CURRENT APPLICATION NUMBER: US/09/729,658B
CURRENT FILING DATE: 2000-12-04
PRIOR PELING DATE: 1999-06-29
PRIOR FILING DATE: 1998-07-09
PRIOR FILING DATE: 1998-12-15
NUMBER OF SEQ ID NOS: 122
SEQ ID NO 4
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 90.8
Matches 355; Conservative
                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Mus musculus
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APPLICANT: Techopp, Jurg
APPLICANT: Techopp, Jurg
APPLICANT: Schneider, Pascal
APPLICANT: Schneider, Pascal
APPLICANT: Holler, Nis
TITLE OF INVENTION: A Biner or an Oligomer of a Dimer, Trimer, Quadromer, or Pentamer
TITLE OF INVENTION: Recombinant Pusion Proteins
FILE REFRENCE: 1708.001051
CURRENT APPLICATION NUMBER: US/10/185,425
CURRENT FILING DATE: 2000-06-28
PRIOR FILING DATE: 2000-12-20
PRIOR FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 24
SNOTWARE: FastSEG for Windows Version 4.0
SEQ ID NO 9
LENGTH: 246
TYPE PRT
CORCANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159 RSKSNEGADGPVKNKKKGKKAGPPGPNGPPGPPGPPGPPGIPGIPGIPGTTVMGPPG 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 ------ESGVKYKKGGLVINETGLYFVYSKVYFRQQSCNNLPLSHKVYMRN-SKY 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 PQDLVMMEGRWMSYCT----TGQMMARSSYLGAVFNLTSADHLYVNVSELSL-VNFEESQ 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219 PPGPPGPPGPPGLQGPSGAADKAGTRENQP----AVVHLQGQGSAIQVK---NDLSGGVL 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 272 NDWSRITMNPKVFKLHPRSGELBVLVDGTYPIYSQV-------EVYYINFTDF 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           318 ASYEVVVDEKPFLQCTRSIETGKTNYNTCYTAGVCLLKARQKIAVKMVHADISINMSKHT 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 OSKSNEGADGPVKNKKKGKKAGPPGPNGPPGPPGPPGPPGPPGIPGIPGIPGIPGIPGTVMGPPG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 25.8%; Score 542; DB 4; Length 246;
Best Local Similarity 47.6%; Pred. No. 1.2e-29;
Matches 118; Conservative 28; Mismatches 64; Indels 38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: DOMAIN; LOCATION: (105)...(246); OTHER INFORMATION: hFas ligand extracellular domain aa 139-281US-10-185-425-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: EDA-Fas ligand fusion protein
APPLICANT: Apotech Research and Development Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (17)...(99)
OTHER INFORMATION: Collagen domain aa 160-242
FEATURE:
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Job time : 116 secs
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OTHER INFORMATION: Linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: DOMAIN
LOCATION: (100)...(104)
OTHER INFORMATION: Linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (1)...(8)
OTHER INFORMATION: Flag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: DOMAIN
LOCATION: (17)...
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Search completed: January 13, 2006, 16:26:34
Job time : 32 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REPERENCE: CLOO1559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 857002
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 915
                                                                                                                                                                                                                                                       17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EAALHSDSQDGHQMALLNFFFPDEKPYSEEESRRVR----RNKRS----KSNEGADGPV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                801
                                                                                                                                                                                                                                                                                                                                                                 -----RRERGAE---SRIGGSGTPGTSGTLSSIGGLD-PDSPITSHIGQPSPKQQPLEPG 119
                                                                                                                                                                                                                                                                                                                                                                                          802 GQIGPRGEDGPEGPRGRAGPTGDPGPSGQAGEKGKLGVPGLP--GYPGRQGPKGSTGFPG 859
                                                                                                                                                                                                                                                                                                                                                                                                                                       120 EAALHSDSQDGHQMALLNFFFPDEKPYSEEESRRVR----RNKRS----KSNEGADGPV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171 -KNKKKKKKKA-----GPPGPNGPPGPPGP---PGPQGPPGIPGIPGIPG-----TTVM 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 PAAAPRERGSQGC----GCGGAPARAGEGNSCLLFLGFFGLSLALHLLTLCCYLELRSEL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   802 GOIGPRGEDGPEGPKGRAGPTGDPGPSGQAGEKGKLGVPGLP--GYPGRQGPKGSTGFPG
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                                                                                                                                                                                                                                                                                                                             755 PIGYPGPRGVKGADGVRGLKGSKGEKGEDG----PPGFKG-DMGLK------GDRGEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        215 GPPGPPGP------PGPQGPPGLQGPSGAADKAGTR 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96;
                                                                                                                                                                                                                                                       96;
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                                                                                                                                                                                                                 12.1%; Score 254; DB 6; Length 1806; 32.0%; Pred. No. 6.2e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 12.1%; Score 254; DB 6; Length 180
Best Local Similarity 32.0%; Pred. No. 6.2e-12;
Matches 93; Conservative 15; Mismatches 87; Indels
                                                                                                                                                                                                                                                     87; Indels
DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                     15; Mismatches
             FILE REFERENCE: CLOO1559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 915, Application US/10995561 Publication No. US20050272054A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                       93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LENGTH: 1806
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-915
                                                                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 93; Conserva
   OF INVENTION:
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                                                                                                                                                                                US-10-995-561-912
                                                                                                                             LENGTH: 1806
                                                                                                        SEQ ID NO 912
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Sequence 910, Application US/10995561
Sequence 910, Application US/1099561
Publication No. US20050272054A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
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                                                                            898 GKPGPKGTSGGDGPPGPPGERGPQGPVGPPGPPGPPGKDPGPPGKDGLPGHPGQRGETGFQ 957
171 -KOKKKKKA-----GPPGPNGPPGPPGP---PGPQGPPGIPGIPGIPG-----TTVM 214
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                                                                                                                                                                                                                                                                                                                                                                   GPPGPPGP-------PGPQGPPGLQGPSGAADKAGTR 244
                                                                                                                                                                                                                                                                         ---- PGPQGPPGLQGPSGAADKAGTR 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) ORGANISM: Homo sapiens
US-10-995-561-910
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Best Local Similarity
                                                                                                                                                                                                                                                                                215 GPPGPPGP--
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APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: HERAPY OF COLON CANCER
FILE REFERENCE: MPMO1-029P2RNM
CURRENT APPLICATION NUMBER: US/11/186, 284
CURRENT FILING DATE: 2005-07-21
PRIOR APPLICATION NUMBER: US/10/301, 822
PRIOR FILING DATE: 2001-11-21
PRIOR FILING DATE: 2001-12-10
PRIOR FILING DATE: 2001-12-10
PRIOR FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: US 60/361, 978
PRIOR APPLICATION NUMBER: US 60/361, 988
PRIOR APPLICATION NUMBER: US 60/361, 988
PRIOR APPLICATION NUMBER: US 60/361, 988
PRIOR PILING DATE: 2002-03-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              874 ------PPG-----ARGLPGPPGSNGNPGPPGPSGSPGKDGPPGPAGNTGAP 914
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Sequence 911, Application US/10995561

Publication No. US200502720541

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS (TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1529
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT PILING DATE: 2004-11-24
SUMMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 911
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28.8%; Pred. No. 3.4e-12;
ive 12; Mismatches 97; Indels 104;
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 93; Conservé
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US-11-186-284-33
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13 PAAAPRERGSQGC----GCGGAPARAGEGNSCLLFLGFFGLSLALHLLTLCCYLELRSEL

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APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 914-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 912, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
PIGYPGPRGVKGADGVRGLKGSKGERGEDG----PPGFKG-DMGLK------GDRGEV 762
                                                                                            GQIGPRGEDGPEGPKGRAGPTGDPGPSGQAGEKGKLGVPGLP--GYPGRQGPKGSTGFPG 820
                                                                                                                                 120 EAALHSDSQDGHQMALLNFFFPDEKPYSEEESRRVR----RNKRS----KSNEGADGPV 170
                                                                                                                                                                      ------PPGAN--GEKGARGVAGKPGPRGQRGPTGPRGSRGARGPT 858
                                                                                                                                                                                                           171 -KNKKKGKKA-----GPPGPNGPPGPPGP---PGPQGPPGIPGIPGIPG-----TTVM 214
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                                                          ----RRERGAE---SRIGGSGTPGTSGTLSSLGGLD-PDSPITSHLGQPSPKQQPLEPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.1%; Score 254; DB 6; Similarity 32.0%; Pred. No. 6e-12; 93; Conservative 15; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 914, Application US/10995561; Publication No. US20050272054A1; GENERAL INFORMATION:
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US-10-995-561-912
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US-10-220-824-8
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APPLICANT: Guillemette, Tracy L.
APPLICANT: Guillemette, Tracy L.
APPLICANT: Sanetkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: HERAPY OF COLON CANCER
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION,
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT,
TITLE OF INVENTION: METHOD FOR 11/186,284
CURRENT APPLICATION NUMBER: US/11/186,284
CURRENT APPLICATION NUMBER: US/10/301,822
PRIOR FILING DATE: 2002-11-21
PRIOR FILING DATE: 2002-11-21
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-03-05
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SUFFRANE: FRALESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                            68 LRRERGAESRIGGSGTPGTSGTLSSIGGLDPDSPITSHIGQPSPKQQPLEPGEAALHSDS 127
                                                                                                                                                                                                                                                                                                             128 ODGHOMALLNFFFPDEKPYSEEESRRVRRNKRSKSNEGADGPVKNKKKGK--KAGPPGPN 185
                                                                                                                                                                                                                                                                                                                                               ----PAGPNGFAGPAGAAGQPGAKGERGAKGPKGENGVVGPT-----GPVGAAGPAGPN 768
                                                                                                                                                                                                                                                                                                                                                                                                    GPPGPPGPPGPQGPPGIPGIPGIPGTTVMGPP-----GPPGPPGPQGPPGLQGPSGAAD 239
                                                                                                                                                                                                                             68 LRRERGAESRIGGSGTPGTSGTLSSLGGLDPDSPITSHLGQPSPKQQPLEPGEAALHSDS 127
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                                                                                                                                           13 PAAAPRERGSQGCGCG----GAPARAGE-GNSCLLFLGFFGLSLALHLLTLCCYLELRSE 67
                                                                                                                                                                                                                                                                        674 ----ARGAHGAVGAPGPAGATGDRGEAGAAGPAGP-----AGPRGSPGERGEVG----
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                                                           Length 1366;
                                                                                                                                                                                   638 PSGLPGERGAAGIPGGKGEKGEPGLRGEIGNP----GRDG----
                                                       12.4%; Score 261; DB 6;
32.9%; Pred. No. 1.3e-12;
iive 10; Mismatches 89;
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Publication No. US20050266493A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
                                                           Query Match
Best Local Similarity 32.99
Matches 80; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo Sapiens
; ORGANISM: Homo sapiens
US-10-821-234-1431
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Sequence 8, Application US/10220824

Publication No. US20050277603A1

GENERAL INFORMATION:
TITLE OF INVENTION: Gene chorapy of rheumatoid arthritis including some price of invention of the process of t
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---ARGAHGAVGAPGPAGATGDRGEAGAAGPAGP-----AGPRGSPGERGEVG---- 718
                                                                                                                                                                                                                                                                                                                      186 GPPGPPGPPGPPGIPGIPGIPGTTVMGPP-----GPPGPPGPPGPPGLQGPSGAAD 239
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APPLICANT: Guillemette, Tracy L. APPLICANT: Kamatkar, Shubhangi APPLICANT: Schlegel, Robert APPLICANT: Monahan, John E. APPLICANT: Thibodeau, Stephen N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 33, Application US/11186284 Publication No. US20050266493A1 GENERAL INFORMATION:
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|1262 NEVAALQPPVVQLH 1275
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Best Local Similarity 28.vv.
Post Local 71; Conservative
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ORGANISM: Homo sapiens
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Sequence 1431.

Sequence 1431.
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APPLICANT: Stache-Crain, Birgit
APPLICANT: Adammani, Susan
APPLICANT: Adammani, Susan
APPLICANT: Andammani, Susan
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
TITLE OF INVENTION: WUMBER: US/10/821,234
CURRENT PILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR APPLICATION NUMBER: US 60/462,047
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SEQ_genes Version 1.0
SEQ ID NO 1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 ALHSDSQDGHQMALLNPPPPDEKPYSEEESRRVRRNKRSKSNEGADGPVKNKKKKKAGP
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; Pred. No. 6.3e-13;
16; Mismatches 80;
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236 GAADKAGTR--ENQPAVVHLQGQ 256
                                        944 GAPGTPGPQGIAGQRGVVGLPGQ 966
                                                                                                                                               Sequence 1096, Application US/10821234 Publication No. US20050255114A1 GENERAL INFORMATION:
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Best Local Similarity 29.7%;
Matches 78; Conservative 16
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                                                                                                           RESULT 6
US-10-821-234-1096
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ORGANISM:
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-----PGADGQPGAKGBPGDAGAKGDAGPPGPAGP----AGPPGPIGNVGAPGA- 861
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                                                                                         Length 1464;
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                                                                                     12.7%; Score 265.5; DB 7;
29.7%; Pred. No. 6.3e-13;
ive 16; Mismatches 80;
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TITLE OF INVENTION: ANTISENSE OLIGONUCLECTIDES
FILE REFERENCE: 06275-254U81
CURRENT APPLICATION NUMBER: US/11/021,603
CURRENT FILING DATE: 2004-12-21
PRIOR APPLICATION NUMBER: PCT/GB00/04741
PRIOR APPLICATION NUMBER: PCT/GB00/04741
PRIOR APPLICATION NUMBER: PCT/GB00/04741
PRIOR FILING DATE: 2000-12-12
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-15
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PATENTIN VET: 4.0
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12.7%; Score 265.5; DB
Best Local Similarity 29.7%; Pred. No. 6.3e-13
Matches 78; Conservative 16; Mismatches 8
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Publication No. US20060003954A1
GENERAL INFORMATION:
                                                                                         Query Match
Best Local Similarity 29.77
Matches 78; Conservative
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                          , ORGANISM: Homo Sapiens
US-11-186-284-28
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US-11-021-603-2
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                                                                       APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Birgit
APPLICANT: Adarmani, Susan
APPLICANT: Andarmani, Susan
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
TITLE OF INVENTION: MOMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR PILNG DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_SEQ_genes Version 1.0
SEQ ID NO 914
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APPLICANT: Tang, Y Tom
APPLICANT: Asundi, Vinod
APPLICANT: Chen, Kui-hong
APPLICANT: Chen, Kui-hong
APPLICANT: Chen, Xiaohong B.
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Jie
APPLICANT: Zhang, Jie
APPLICANT: Zhou, Ping
APPLICANT: Zhou, Ping
APPLICANT: Dramac, Radoje T.
TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REFERENCE: 785CIP4CN
CURRENT APPLICANTON NUMBER: US/11/000,463
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PRIOR APPLICATION NUMBER: 10/291,265
PRIOR FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: PCT/US01/02623
PRIOR FILING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 09/922,279
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Publication No. US20050266423A1
GENERAL INFORMATION:
Sequence 914, Application US/10821234 Publication No. US20050255114A1 GENERAL INFORMATION:
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Best Local Similarity 31.2%
Matches 85; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: MILEMING FURGACCULCARS, INC.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Schlegel, Robert
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Monahan, John E.
APPLICANT: MONER: US/11/186,284
CURRENT APPLICATION NUMBER: US/10/301,822
PRIOR PILING DATE: 2002-01-21
PRIOR PELING DATE: 2002-01-21
PRIOR PELING DATE: 2002-12-10
PRIOR PLING DATE: 2002-03-05
PRIOR PLING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 28
LENGTH: 1464
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PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
PRIOR APPLICATION NUMBER: 09/617,746
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR APPLICATION NUMBER: 09/631,451
PRIOR APPLICATION NUMBER: 09/633,870
PRIOR APPLICATION NUMBER: 09/633,870
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 944
SOFTWARE: PSELSEQ for Windows Version 3.0
SEQ ID NO 243
LENGTH: 1464
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US-11-000-463-243
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1051 GHPGPPGPPGEQGLPGLAGKEGTK-GDPGPAGLPGK 1085
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Sequence 2, Appli
Sequence 1096, Ap
Sequence 1431, Appl
Sequence 31, Appli
Sequence 33, Appli
Sequence 931, Appli
Sequence 911, Appli
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Sequence 914, App
Sequence 243, App
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119.245 Million cell updates/sec
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2: /cgn2_6/ptodata/2/pubpaa/USO6 NEW FUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO7 NEW FUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO7 NEW FUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO8 NEW FUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO8 NEW FUB.pep:*
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                         GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd
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US-11-186-284-28
US-11-021-621-629-2
US-10-821-224-1431
US-10-821-224-1431
US-10-821-224-33
US-10-220-824-3
US-10-995-561-911
US-10-995-561-915
US-10-995-561-915
US-10-995-561-915
US-11-186-284-39
US-11-124-368A-329
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Sequence 532, App
Sequence 8, Appli
Sequence 2, Appli
Sequence 6, Appli
Sequence 10, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 14, Appli
Sequence 16, Appli
Sequence 16, Appli
Sequence 11, Appli
US-11-096-070-12

US-10-995-561-532

US-11-096-070-8

US-11-096-070-2

US-11-096-070-6

US-11-096-070-6

US-11-096-070-10

US-10-096-070-4

US-10-096-070-3

US-10-131-234-1438

US-10-131-234-1438

US-11-143-986-8

US-11-143-986-9

US-11-143-985-31

US-11-143-985-31
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       221.5
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203.5
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189
176.5
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ALIGNMENTS

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Sequence 1182. Application US/10821234
; Sequence 1182. Application US/10821234
; Publication No. US20050255114A1
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; TITLE OF INVENTION: WHOMER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SEQ ID NOS: 1704
; SEQ ID NOS: 1704
; SEQ ID NOS: 1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 RGAESRIGGSGTPGTSGTLSSLGGLDPDSPITSHLGQPSPKQQPLEPGEAALHSDSQDGH 131
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Best Local Similarity 30.1
Matches 83; Conservative
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US-10-821-234-1182
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